

GenCore version 5.1.7
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DOM protein - protein search, using sw model

Run on: April 20, 2006, 09:35:12 ; Search time 109.906 Seconds
 (without alignments)

971.459 Million cell updates/sec

Title: US-10-634-108-4

Perfect score: 13.03

Sequence: 1 MRPQSPAASPORLQRGNLLL.....GDASTGWSVRII1B1LPK 243

Scoring table: BLOSUM62

Gapext: Gapext 0.5

Scanned: 2443163 seqs, 433378781 residues

Searched: 2443163 seqs, 433378781 residues

Total number of hits satisfying chosen parameters: 2443163

Post-processing: Minimum Match 0% Maximum Match 100%
 Listing First 45 summaries
Database : A Geneseg 21:
RESULT 1
AAB36667
 ID AAB36667 standard; protein; 243 AA.
 XX

1: - geneseqP1980s;* AC AAB36667;
 2: geneseqP1990s;* XX
 3: geneseqP2000s;* DT 14-MAR-2001 (first entry)
 4: geneseqP2001s;* XX
 5: geneseqP2002s;* Human secretary protein TGC-628 SEQ ID NO:7.
 6: geneseqP2003as;* XX
 7: geneseqP2003bs;* Human; secretory protein; cancer; immune disorder; infectious disease;
 8: geneseqP2004s;* lung function disorder; liver function disorder; antinflammatory;
 9: geneseqP2005s;* gastrointestinal disorder; cytotoxic; haemato poetic; anticoagulant;
 cell immunomodulatory; hepatotropic; cell proliferation-stimulant;
 cell migratory agent; cell differentiation-inducer.
 XX Homo sapiens.

SUMMARIES

Result No.	Score	Query	Match Length	ID	DB	Description
	Score	Match Length	ID	DB	Description	
1	1303	100.0	243	4	AAB36667	Human sec
2	1303	100.0	243	5	ABG95640	Human ova
3	1303	100.0	243	5	ABJ05534	Breast ca
4	1303	100.0	243	5	Abb80978	Human REM
5	1303	100.0	243	6	Abr58546	Human can
6	1303	100.0	243	6	ABR48227	Human bla
7	1303	100.0	243	6	Abg75758	Human REM
8	1303	100.0	243	6	ABU56607	Lung Canc
9	1303	100.0	243	7	ADB80510	Ovarian c
10	1303	100.0	243	7	ADN39855	Cancer/an
11	1303	100.0	243	7	ADN38732	Cancer/an
12	1303	100.0	243	8	ADL70254	Ad170254
13	1303	100.0	243	8	ADU23513	Alternati
14	1303	100.0	243	8	ADU06493	Ad06493
15	1303	100.0	243	9	AEB28819	Novel bro
16	1303	100.0	278	3	AAB08856	Amino aci
17	1303	100.0	278	4	AAM25746	Aam25746
18	1303	100.0	278	5	ABG96338	Human ova
19	1303	100.0	278	6	ABR47627	Abra7627
20	1303	100.0	278	9	ADZ251345	Adz251345
21	1300	99.8	243	3	AAY915249	Aay915249
22	1300	99.8	243	8	ADL71601	Novel
23	1300	99.8	278	5	ABP68631	Human pro
24	1298	99.6	243	6	ABT37031	Abt37031

CC which are used in the exemplification of the present invention
 XX Sequence 243 AA;

Query Match 100.0%; Score 1303; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT PT
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.

XX Disclosure: Page 252: 481pp; English.

Qy 1 MRPOGPAASPORLQLLQLQLPAPSASBPKQKQAKQLRQEVDLYNGMCLQGPAA 60
 Db 1 MRPOGPAASPORLQLLQLQLPAPSASBPKQKQAKQLRQEVDLYNGMCLQGPAA 60
 Qy 61 GVPGRDGSPGANGIPETPGIPGRDKGBCRESFESWTPNPKQCSWSSLNYGIDL 120
 Db 61 GVPGRDGSPGANGIPETPGIPGRDKGBCRESFESWTPNPKQCSWSSLNYGIDL 120
 Qy 121 GKIAECKFTKMRNSALRVLFSGSLRLKCRNACCORWYFTENGABCSPGPLPIEATIYLQDQ 180
 Db 121 GKIAECKFTKMRNSALRVLFSGSLRLKCRNACCORWYFTENGABCSPGPLPIEATIYLQDQ 180
 Qy 181 GSPEMNISTINHRTSSVEGLCEGIGAGIVDAIWGTCDYKPGDASTGNNSVRIIE 240
 Db 181 GSPEMNISTINHRTSSVEGLCEGIGAGIVDAIWGTCDYKPGDASTGNNSVRIIE 240
 Qy 241 LPK 243
 Db 241 LPK 243

RESULT 2
 ABG96340 standard; protein; 243 AA.
 ID ABG96340
 AC ABG96340;
 XX DT 11-DEC-2002 (first entry)

XX Human ovarian cancer marker M450.
 DE Human ovarian cancer marker M450.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; cerebral disorder; non-tuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; histological type; carcinogenic; ovarian cancer marker.

XX Homo sapiens.

PN WO200271928-A2.

XX PD 19-SEP-2002.
 XX PP 14-MAR-2002; 2002WO-US007826.

XX PR 14-MAR-2001; 2001US-0276025P.
 PR 14-MAR-2001; 2001US-0276025P.
 PR 10-AUG-2001; 2001US-0311732P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 26-SEP-2001; 2001US-0324967P.
 PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.

XX PA (MILL-) MILLENIUM PHARM INC.
 XX PD ABJ05554 standard; protein; 243 AA.

XX AC ABJ05554;

XX PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;

PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Viebey PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;

DR WPI; 2002-723277/78.
 DR N-PSDB; ABS76436.

XX Assessing whether a patient is afflicted with ovarian cancer, useful in
 XX PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.

XX Disclosure: Page 252: 481pp; English.

XX The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be particularly useful with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the invention

XX SQ Sequence 243 AA;

XX Query Match 100.0%; Score 1303; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 MRPOGPAASPORLQLLQLQLPAPSASEIPKGKQAKQLRQEVDLYNGMCLQGPAA 60
 Db 1 MRPOGPAASPORLQLLQLQLPAPSASEIPKGKQAKQLRQEVDLYNGMCLQGPAA 60
 Qy 61 GVPGRDGSPGANGIPETPGIPGRDKGBCRESFEESWTPNPKQCSWSSLNYGIDL 120
 Db 61 GVPGRDGSPGANGIPETPGIPGRDKGBCRESFEESWTPNPKQCSWSSLNYGIDL 120
 Qy 121 GKIAECKFTKMRNSALRVLFSGSLRLKCRNACCORWYFTENGABCSPGPLPIEATIYLQDQ 180
 Db 121 GKIAECKFTKMRNSALRVLFSGSLRLKCRNACCORWYFTENGABCSPGPLPIEATIYLQDQ 180
 Qy 181 GSPEMNISTINHRTSSVEGLCEGIGAGIVDAIWGTCDYKPGDASTGNNSVRIIE 240
 Db 181 GSPEMNISTINHRTSSVEGLCEGIGAGIVDAIWGTCDYKPGDASTGNNSVRIIE 240
 Qy 241 LPK 243
 Db 241 LPK 243

RESULT 3
 ABJ05554
 ID ABJ05554

XX ABJ05554 (First entry)
 XX DT 14-NOV-2002
 XX DE Breast cancer-associated protein 19.
 XX KW Breast cancer; breast cancer-associated gene sequence; drug development;
 XX KW pharmacogenetics; biosensor development.
 XX PT

OS Unidentified.
 XX
 PN WO200259377-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002242.
 XX
 PR 24-JAN-2001; 2001US-0263965P.
 PR 02-FEB-2001; 2001US-0265947P.
 PR 09-APR-2001; 2001US-00829472.
 PR 09-APR-2001; 2001US-0282658P.
 PR 04-MAY-2001; 2001US-0285943P.
 PR 29-MAY-2001; 2001US-0294443P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack DH, Gish KC, Afar D;
 XX
 DR WPI; 2002-583738/62.
 XX
 DR N-PSDB; AB107711.
 XX
 PT Detecting a breast cancer-associated transcript in a patient's cell,
 PT useful for diagnosing breast cancer, comprises contacting a biological
 PT sample with a polynucleotide that selectively hybridizes with breast
 PT cancer nucleic acids.
 XX
 PS Disclosure; Page 364; 414pp; English.
 XX
 CC The invention comprises a method of detecting a breast cancer-associated
 CC transcript in a cell from a patient. The method of the invention involves
 CC contacting a biological sample from the patient with a nucleotide that
 CC hybridises to one of the 69 breast cancer-associated gene sequences shown
 CC in the specification. The method of the invention is useful in the
 CC diagnosis or prognosis of breast cancer, and for detecting genes that are
 CC up or down-regulated in breast cancer cells. Genes identified by the
 CC method of the invention can be used in diagnostic purposes and also as
 CC targets for screening for therapeutic compounds that modulate breast
 CC cancer (e.g. hormones or antibodies). Identification of genes that are
 CC over or under expressed in breast cancer can additionally provide high-
 CC resolution, high-sensitivity datasets which can be used in the areas of
 CC diagnostics, therapeutics, drug development, pharmacogenetics, protein
 CC structure and biosensor development. Amino acid sequences ABJ05536 -
 CC ABJ05604 represent the proteins encoded by the 69 breast cancer-
 CC associated genes of the invention.
 XX
 SQ Sequence 243 AA:
 Query Match 100.0%; Score 1303; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60
 Db 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60
 Qy 61 GVPGRDGSPGANGIPCTPGIPGRDGPKGEKGCRCLRESFESWTNPYKQCSNSLNYGID 120
 Db 61 GVPGRDGSPGANGIPCTPGIPGRDGPKGEKGCRCLRESFESWTNPYKQCSNSLNYGID 120
 Qy 121 GKIAECPTPKRSNSALRVLGSLRILRKCRMACQWYFTNGAECGSPPLDIEATIYLDDQ 180
 Db 121 GKIAECPTPKRSNSALRVLGSLRILRKCRMACQWYFTNGAECGSPPLDIEATIYLDDQ 180
 Qy 181 GSPEMNSTINIRHTSSVYGLCEFGIGAGIVDVAIWVGTCSDYPKGDASTGNNVSRIIEE 240
 Db 181 GSPEMNSTINIRHTSSVYGLCEFGIGAGIVDVAIWVGTCSDYPKGDASTGNNVSRIIEE 240
 Qy 241 LPK 243
 Db 241 LPK 243

RESULT 4
 ABB80978
 ID ABB80978 standard; protein; 243 AA.
 XX
 AC ABB80978;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human REMODELIN polypeptide.
 XX
 KW REMODELIN; pulmonary; vasotropic; cytostatic; osteopathic; collagen;
 KW gene therapy; bone; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200242487-A2.
 XX
 PD 30-MAY-2002.
 XX
 PR 19-OCT-2001; 2001WO-US050940.
 XX
 PR 19-OCT-2000; 2000US-00629081.
 XX
 PA (MAIN-) MAINE MEDICAL CNT RES INST.
 XX
 PI Linder V, Friesel R;
 XX
 DR WPI; 2002-590472/63.
 DR N-PSDB; ASN86481.
 XX
 PT New mammalian REMODELIN polypeptide for diagnosing arterial restenosis,
 PT negative remodeling, fibrosis, collagen disease, and bone disease in a
 PT mammal.
 XX
 PS Claim 5; Fig 4B; 187pp; English.
 XX
 CC The invention relates to mammalian REMODELIN polypeptides and encoding
 CC polynucleotides. REMODELIN is used to diagnose arterial restenosis,
 CC negative remodeling or fibrosis, bone disease such as osteogenesis
 CC imperfecta (OI), dystrophic epidermolysis bullosa (DEB) and Bethlem myopathy in a mammal. The polynucleotides are
 CC used to affect cellular gene expression in a mammal, where the cellular
 CC gene is from transforming growth factor (TGF)-beta1, collagen III, collagen IV, bone morphogenic protein
 CC osteopontin, biglycan, alkaline phosphatase or bone morphogenic protein
 CC 4. The expression of osteopontin is dependent on Cbfa1. Compositions
 CC comprising antisense REMODELIN sequences are useful for treating diseases
 CC mediated by abnormal expression of a REMODELIN molecule in a human such
 CC as impaired wound healing, fibrosis of an organ, ectopic ossification, or
 CC hypertrophic scar formation. REMODELIN is useful in the development of
 CC cellular signaling, adventitial fibrosis, negative remodeling and arterial
 CC restenosis, smooth muscle cell proliferation, and arterial remodeling and
 CC useful in gene therapy. REMODELIN is useful for elucidating the function
 CC of REMODELIN molecules in a cell, to identify a compound that affects
 CC REMODELIN expression and/or TGF-beta1 signaling, as a potential
 CC therapeutic drug candidate for arterial restenosis, anti-cancer therapy,
 CC to promote or inhibit wound healing, to inhibit scar tissue or keloid
 CC formation, to promote bone fracture healing, and to increase or decrease
 CC expression of REMODELIN in mammal. It is also useful for producing recombinant cell and transgenic non-human mammals which are useful tools
 CC for the study of REMODELIN action, for identifying novel diagnostics and
 CC therapeutics for treatment, and for elucidating the cellular roles of
 CC REMODELIN. The present sequence represents a human REMODELIN polypeptide
 XX
 SQ Sequence 243 AA:
 Query Match 100.0%; Score 1303; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60
 Db 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60
 Qy 121 GKIAECPTPKRSNSALRVLGSLRILRKCRMACQWYFTNGAECGSPPLDIEATIYLDDQ 180
 Db 121 GKIAECPTPKRSNSALRVLGSLRILRKCRMACQWYFTNGAECGSPPLDIEATIYLDDQ 180
 Qy 181 GSPEMNSTINIRHTSSVYGLCEFGIGAGIVDVAIWVGTCSDYPKGDASTGNNVSRIIEE 240
 Db 181 GSPEMNSTINIRHTSSVYGLCEFGIGAGIVDVAIWVGTCSDYPKGDASTGNNVSRIIEE 240
 Qy 241 LPK 243
 Db 241 LPK 243

Query Match 100.0%; Score 1303; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60
 Db 1 MRPOGPASPORLRLILLIQLPAPSASEIPKGKQKAQRQREVVDLYNGMCLQGPA 60

Qy	61 GVPGRDGSPGANGIPGTPGTGIPGRDGFKGKBCLRESFEESWTNYKQCSWSSLNYGIDL	CC therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in screening, particularly for identifying agents for treating these pathologies
Db	61 GVPGRDGSPGANGIPGTPGTGIPGRDGFKGKBCLRESFEESWTNYKQCSWSSLNYGIDL	CC
Db	121 GKIAECTFTKMRNSALRVLFGSLRLKCRMACCQBWYPTNGAECGSPLPBIAIYLQDQ	CC
Qy	121 GKIAECTFTKMRNSALRVLFGSLRLKCRMACCQBWYPTNGAECGSPLPBIAIYLQDQ	CC
Db	121 GKIAECTFTKMRNSALRVLFGSLRLKCRMACCQBWYPTNGAECGSPLPBIAIYLQDQ	CC
Qy	181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE	XX
Db	181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE	XX
Qy	241 LPK 243	Sequence 243 AA;
Db	241 LPK 243	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
<hr/>		
RESULT 5		
ID	ABR5546 standard; protein; 243 AA.	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
AC	ABR5546;	Qy 1 MRPQQPAASPORLQLLQLQDAPSSASEIPIKGKOKAQLRQEUVDLYNGMCLQGPA 60
XX		Db 1 MRPQQPAASPORLQLLQLQDAPSSASEIPIKGKOKAQLRQEUVDLYNGMCLQGPA 60
DT	09-JUL-2003 (first entry)	Qy 61 GVPGRDGSPGANGIPGTPGTGIPGRDGFKGKBCLRESFEESWTNYKQCSWSSLNYGIDL 120
XX		Db 61 GVPGRDGSPGANGIPGTPGTGIPGRDGFKGKBCLRESFEESWTNYKQCSWSSLNYGIDL 120
DE	Human cancer related protein SEQ ID NO:203.	Qy 61 GKIACETFTKMRNSALRVLFGSLRLKCRMACCQBWYPTNGAECGSPLPBIAIYLQDQ 180
XX		Db 61 GKIACETFTKMRNSALRVLFGSLRLKCRMACCQBWYPTNGAECGSPLPBIAIYLQDQ 180
KW	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.	Qy 121 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE 240
XX		Db 121 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE 240
OS	Homo sapiens.	Qy 181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE 240
XX		Db 181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVRIIEE 240
PN	WO2003025138-A2.	Qy 241 LPK 243
XX		Db 241 LPK 243
PD	27-MAR-2003.	RESULT 6
XX		ABR48227 standard; protein; 243 AA.
PF	17-SEP-2002; 2002WO-US029560.	ID ABR48227
XX		XX ABR48227;
PR	17-SEP-2001; 2001US-0323469P.	AC
PR	20-SEP-2001; 2001US-0323468P.	XX DT 12-JUN-2003 (first entry)
PR	13-NOV-2001; 2001US-0350666P.	XX DB Human bladder cancer associated protein sequence SEQ ID NO:175.
PR	08-FEB-2002; 2002US-0355145P.	XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
PR	08-FEB-2002; 2002US-0355257P.	XX Homo sapiens.
PR	12-APR-2002; 2002US-0372246P.	XX WO200303906-A2.
PA	(EOSB-) EOS BIOTECHNOLOGY INC.	XX PN 16-JAN-2003.
Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;		XX PF 03-JUL-2002; 2002WO-US021338.
PI	PI Zlotnik A;	XX XX
XX	WPI; 2003-354600/33.	XX PR 03-JUL-2001; 2001US-0302814P.
DR	DR ACC72666.	XX PR 03-AUG-2001; 2001US-0310099P.
N-PSDB;		XX PR 08-NOV-2001; 2001US-0344705P.
XX		XX PR 13-NOV-2001; 2001US-0351666P.
PT	New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.	XX PR 12-APR-2002; 2002US-0372246P.
PT	Claim 12; Page 736; 767pp; English.	XX XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX	The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or	XX PI Mack DH, Aziz N;
XX		XX XX DR WPI; 2003-201532/19.
XX		XX DR N-PSDB; ACC51043.
XX	Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.	XX XX PS Claim 10; Page 289-290; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR41146 to ABR48242. Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications.

XX Sequence 243 AA;

	Query Match	Best Local Similarity	Length	Score	Pred.	No.	Mismatches	Indels	Gaps	0;
Qy	1 MRPQGPAASPORLRLGLLILQLPAPSSASBPKGKQKAOLRQEVVDLYNGMCLQGPA	100.0%	243	1303	DB 6;	Length 243;	0;	0;	0;	;
Dy	1 MRPQGPAASPORLRLGLLILQLPAPSSASBPKGKQKAOLRQEVVDLYNGMCLQGPA	100.0%	243	1303	DB 6;	Length 243;	0;	0;	0;	;
Qy	61 GVPGRDGGPGANGTPGTGIPGRDGFKCBEKGCLRESFESWTPNYQCSWSNLNGIDL	100.0%	120	120	DB 120	Length 120	0;	0;	0;	;
Dy	61 GVPGRDGGPGANGTPGTGIPGRDGFKCBEKGCLRESFESWTPNYQCSWSNLNGIDL	100.0%	120	120	DB 120	Length 120	0;	0;	0;	;
Qy	121 GKAECTFTKMRNSNALSRLVLFSGSLRLKCRNACQQRMFTFNGAECGPLPIEAITYLDQ	100.0%	180	180	DB 180	Length 180	0;	0;	0;	;
Dy	121 GKAECTFTKMRNSNALSRLVLFSGSLRLKCRNACQQRMFTFNGAECGPLPIEAITYLDQ	100.0%	180	180	DB 180	Length 180	0;	0;	0;	;
Qy	181 GSPBMNSTINHRTSSVGLCBGIGAGLYDVAIWVGTSYDYPKGDASTGMNSVSRIIEE	100.0%	240	240	DB 240	Length 240	0;	0;	0;	;
Dy	181 GSPBMNSTINHRTSSVGLCBGIGAGLYDVAIWVGTSYDYPKGDASTGMNSVSRIIEE	100.0%	240	240	DB 240	Length 240	0;	0;	0;	;
Qy	241 LPK 243	100.0%	243	243	DB 243	Length 243	0;	0;	0;	;
Dy	241 LPK 243	100.0%	243	243	DB 243	Length 243	0;	0;	0;	;

RESULT 7

ID ABG75758 standard; protein: 243 AA.
 XX ABG75758;
 XX DT 28-APR-2003 (first entry)
 XX Human REMODELIN protein.
 XX Human; adventitia-inducible; REMODELIN; REMODELIN; TGF-beta; TGF-beta; transforming growth factor beta; adventitia; vascular remodelling; restenosis; vascular injury; antisense therapy; bone formation; cartilage formation; osteogenesis imperfecta; Ehlers myopathy; dystrophic epidermolysis bullosa; negative remodelling; wound healing; arterial stenosis; fibrosis; calcification; transplant; heart valve transplant; osteopathic; antiarteriosclerotic; pulmonary.

XX Homo sapiens.
 XX OS Homo sapiens.
 XX PN US2002161211-A1.
 XX PD 31-OCT-2002.
 XX PP 19-OCT-2001; 2001US-00045992.
 XX PR 19-OCT-2000; 2000US-00692081.
 XX RESULT 8
 XX ABU56607
 ID ABU56607 standard; protein: 243 AA.
 XX AC ABU56607;

XX	02-APR-2003	(first entry)	Qy	121 GKIACETFTKMRNSALRVLFLSGSIRLKCERNACCRWYFTENGACSGPLPIEAIIYLDQ 180
DT	Lung cancer-associated polypeptide #200.		Db	121 GKIACETFTKMRNSALRVLFLSGSIRLKCERNACCRWYFTENGACSGPLPIEAIIYLDQ 180
XX			XX	
XX	Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hyperensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.		Qy	181 GSPEMNSTINTHRTSSVEGLCEGIGAGLYDVAIWGTCSDPKGDASTGWNNSVRIIEE 240
KW			Db	181 GSPEMNSTINTHRTSSVEGLCEGIGAGLYDVAIWGTCSDPKGDASTGWNNSVRIIEE 240
KW			Qy	241 LPK 243
KW			Db	241 LPK 243
OS	Unidentified.		OS	
XX	WO200286443-A2.		PN	
XX	PD 31-OCT-2002.		PD	RESULT 9
XX	PP 18-APR-2002; 2002WO-US012476.		ID	ADB80510 standard; protein; 243 AA.
XX	PR 18-APR-2001; 2001US-0284770P.		XX	
PR	10-MAY-2001; 2001US-0290492P.		AC	ADB80510;
PR	09-NOV-2001; 2001US-0339245P.		XX	
PR	13-NOV-2001; 2001US-0350666P.		DT	04-DEC-2003 (first entry)
PR	29-NOV-2001; 2001US-0334370P.		XX	Ovarian cancer-associated protein #37.
PR	12-APR-2002; 2002US-0372246P.		DE	
XX	(EOSB-) EOS BIOTECHNOLOGY INC.		XX	cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
PA			KW	
PA	PI Aziz N, Murray R;		XX	KW
PA	XX		OS	Homo sapiens.
PA	DR WPI; 2003-093161/08.		XX	
PA	DR N-PSDB; A8X76336.		PN	WO2002102235-A2.
XX	XX		PD	27-DEC-2002.
XX	Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.		XX	18-JUN-2002; 2002WO-US019297.
PT	Claim 27; Page 337; 453pp; English.		XX	18-JUN-2001; 2001US-0299234P.
PT	The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hyperensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56108-ABU56745 represent lung cancer-associated polypeptides of the invention		PR	18-JUN-2001; 2001US-031287P.
PT	Sequence 243 AA;		PA	05-SEP-2001; 2001US-0317444P.
PT	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PR	13-NOV-2001; 2001US-0350666P.
PS	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PR	12-APR-2002; 2002US-0372246P.
XX	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PA	(EOSB-) EOS BIOTECHNOLOGY INC.; Mack DH, Gish KC;
CC	CC		PI	XX
CC	CC		XX	WPI; 2003-167431/16.
CC	CC		DR	N-PSDB; ADB80509.
CC	CC		XX	Detecting an ovarian cancer-associated transcript in a cell from a cell from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
CC	CC		XX	PT
CC	CC		XX	Detecting an ovarian cancer-associated transcript in a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancer.
CC	CC		XX	PT
CC	CC		XX	Detecting an ovarian cancer-associated transcript in a cell from a patient with a polynucleotide that selectively hybridizes to a sequence that is at least 80 % identical to any one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancer, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
CC	CC		XX	Claim 13; Page 299; 332pp; English.
CC	CC		XX	The invention relates to a method of detecting an ovarian cancer-associated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is at least 80 % identical to any one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancer, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
CC	CC		XX	Query Match 100.0%; Score 1303; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	CC		DB	1 MRPGQGSPASPORLGLLILLQLPAPSASRIPKGKQKAQLQRQEVDLYNGMCLQGP 60
CC	CC		DB	1 MRPGQGSPASPORLGLLILLQLPAPSASRIPKGKQKAQLQRQEVDLYNGMCLQGP 60
CC	CC		Qy	61 GVPGRDGSPGANGIPGTPGIPGRDGFKEKGCCLRESFEWTNPYKQCSWSSLNYGIDL 120
CC	CC		Db	61 GVPGRDGSPGANGIPGTPGIPGRDGFKEKGCCLRESFEWTNPYKQCSWSSLNYGIDL 120
CC	CC		Qy	61 GVPGRDGSPGANGIPGTPGIPGRDGFKEKGCCLRESFEWTNPYKQCSWSSLNYGIDL 120
CC	CC		Db	61 GVPGRDGSPGANGIPGTPGIPGRDGFKEKGCCLRESFEWTNPYKQCSWSSLNYGIDL 120
CC	CC		Query Match	100.0%; Score 1303; DB 7; Length 243;
CC	CC		SQ	Sequence 243 AA;

OS	Homo sapiens.	Qy	121 GKIACCTFTKMRNSNALSRLVLFSGSURLKCRNACCCRWTFTNGACBESGPLPIEATIYLDQ 180
XX	XX	Db	121 GKIACCTFTKMRNSNALSRLVLFSGSURLKCRNACCCRWTFTNGACBESGPLPIEATIYLDQ 180
PN	WO2003042661-A2.	Qy	181 GSPENMNSTINHTRSSEVGICGAGLVDVIAWYGTCSDPKGDASTGWNNSVRIIEE 240
PD	22-MAY-2003 .	Db	181 GSPENMNSTINHTRSSEVGICGAGLVDVIAWYGTCSDPKGDASTGWNNSVRIIEE 240
XX	XX	Qy	181 GSPENMNSTINHTRSSEVGICGAGLVDVIAWYGTCSDPKGDASTGWNNSVRIIEE 240
PF	13-NOV-2002 ; 2002WO-US036810.	Db	181 GSPENMNSTINHTRSSEVGICGAGLVDVIAWYGTCSDPKGDASTGWNNSVRIIEE 240
XX	PR 13-NOV-2001 ; 2001US-0350666P.	Qy	241 LPK 243
PR	21-NOV-2001 ; 2001US-0332454P.	Db	241 LPK 243
PR	29-NOV-2001 ; 2001US-0334393P.	Qy	241 LPK 243
PR	03-DEC-2001 ; 2001US-035394P.	Db	241 LPK 243
PR	14-DEC-2001 ; 2001US-034076P.		
PR	08-JAN-2002 ; 2002US-0347211P.		
PR	10-JAN-2002 ; 2002US-034724P.		
PR	08-FEB-2002 ; 2002US-035523P.		
PR	13-FEB-2002 ; 2002US-0356714P.		
PR	20-FEB-2002 ; 2002US-0359077P.		
PR	29-MAR-2002 ; 2002US-0368809P.		
PR	04-APR-2002 ; 2002US-037010P.		
PR	12-APR-2002 ; 2002US-037224P.		
PR	05-JUN-2002 ; 2002US-0386614P.		
PR	16-JUL-2002 ; 2002US-0396839P.		
PR	22-JUL-2002 ; 2002US-039775P.		
PR	22-JUL-2002 ; 2002US-039785P.		
PR	09-SEP-2002 ; 2002US-0409450P.		
XX	(EOS-) EOS BIOTECHNOLOGY INC.	OS	Homo sapiens.
XX	PA	XX	XX
PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezzi PA;	PN	WO2004016636-A1.
PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;	XX	XX
XX	DR; WPI; 2003-468649/44.	PD	26-FEB-2004.
DR	N-PSDB; ADL70254;	XX	XX
XX	Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosis or treating cancer, comprises detecting a nucleic acid in a biological sample.	PF	14-AUG-2003 ; 2003WO-KR001653.
PT	XX	XX	XX
PT	XX	XX	XX
PT	XX	XX	XX
PT	XX	XX	XX
XX	Claim 12; SEQ ID NO 50; 138pp; English.	XX	XX
XX	The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosis and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularization syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.	XX	XX
PS	XX	XX	XX
XX	The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosis and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularization syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.	XX	XX
XX	Query Match 100.0%; Score 1303; DB 7; Length 243;	XX	XX
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;	XX	XX	XX
Matches 243; Conservative 0;	XX	XX	XX
Qy 1 MRPQGPASPORLGRILLILQLPAPSASAEIPKGKQKAOLRQREVVDLYNGMCLQGPAA 60	CC	CC	CC
Db 1 MRPQGPASPORLGRILLILQLPAPSASAEIPKGKQKAOLRQREVVDLYNGMCLQGPAA 60	CC	CC	CC
Qy 61 GYPGRDGSPPGANGIPGTPGIPIRDGPXGEKGBCLRSFEESWTNTYKQCSMSSINYGIDL 120	CC	CC	CC
Db 61 GYPGRDGSPPGANGIPGTPGIPIRDGPXGEKGBCLRSFEESWTNTYKQCSMSSINYGIDL 120	CC	CC	CC

DR WPI; 2004-786403/78.
 XX N-PSDB; ADU06006.
 PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial
 cancer and in screening for therapeutic and diagnostic agents.
 PT XX
 PS Claim 2; SEQ ID NO 717; 1381pp; German.
 XX
 CC This invention relates to a novel isolated nucleic acid associated with
 bronchial cancer comprising 489 defined sequences given in the
 specification. The invention may be useful for the production of
 compounds with a cytostatic activity through the inhibition of expression
 or activity of tumour-associated proteins. The novel DNA sequences and
 the proteins/peptides encoded by them are used for detecting bronchial
 cancer or determining the risk of developing it and to screen for
 specific binding partners of the DNA or protein sequences, where the
 binding partners are potentially useful as agents for treating or
 diagnosing bronchial cancer. The DNA or protein sequences can also be
 used for prognosis, detection of metastases and for secondary treatment
 (of tumours that have been stabilised or are no longer detectable).
 CC Detecting abnormal expression of the DNA sequences provides early
 diagnosis of bronchial cancers. The present sequence is that of a protein
 encoded by a novel bronchial cancer-associated human gene sequence of the
 invention.
 XX
 SQ Sequence 243 AA;
 Query Match 100.0%; Score 1303; DB 8; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Gaps 0;
 Db 1 MRPQGPAAASPORLRLGILLLQLPAPSASEBIPKGOKAQLRREVVDLYNGMCLQGPAA 60
 Db 1 MRPQGPAAASPORLRLGILLLQLPAPSASEBIPKGOKAQLRREVVDLYNGMCLQGPAA 60
 Qy 61 GVPGRDGSPGANGIPTGPICPORDGPKGKEGBCLRESSEESWTNYKOCWSSSLNYGIDL 120
 Db 61 GVPGRDGSPGANGIPTGPICPORDGPKGKEGBCLRESSEESWTNYKOCWSSSLNYGIDL 120
 Qy 121 GKIAECKTFKRSNLSALRVFGSLRLKCRNACQWYFTPNAGBCGPPIEAITYLDQ 180
 Db 121 GKIAECKTFKRSNLSALRVFGSLRLKCRNACQWYFTPNAGBCGPPIEAITYLDQ 180
 Qy 181 GSPEMNSTINHRTSSVEGLCGBIGAGLVDAIWGTCSDFPKGDASTGNNSVRIIE 240
 Db 181 GSPEMNSTINHRTSSVEGLCGBIGAGLVDAIWGTCSDFPKGDASTGNNSVRIIE 240
 Qy 241 LPK 243
 Db 241 LPK 243
 RESULT 15
 AEB28819 standard; protein; 243 AA.
 XX AC AEB28819;
 XX DT 08-SEP-2005 (first entry)
 XX Human CTHRC1 protein SEQ ID NO:4.
 XX collagen triple helix repeat containing 1; CTHRC1; vulnerability;
 KW anti-inflammatory; respiratory-gen.; vasoconstrictor; fibrosis;
 KW restenosis;
 KW wound healing; scarring.
 OS Homo sapiens.
 PN US2005147602-A1.
 XX PD 07-JUL-2005.
 XX PP 10-SEP-2004; 2004US-00939233.
 YY

XX PR 19-OCT-2000; 2000US-00692081.
 XX PR 19-OCT-2001; 2001US-0005992.
 PR 18-SEP-2003; 2003US-0505933P.
 PR 18-SEP-2003; 2003US-0504107P.
 XX PA (MAIN-) MAINE MEDICAL CENT RES INST.
 XX PI Lindner V;
 XX WPI; 2005-478076/48.
 DR N-PSDB; AEB28834.
 XX Novel isolated polypeptide comprising human cleaved collagen triple helix
 repeat containing 1 (CTHRC1) or isolated murine CTHRC1 polypeptide,
 PT useful for treating or preventing disease mediated by collagen matrix
 PT production e.g. fibrosis.
 XX PS Example 1; SEQ ID NO 4; 115pp; English.
 XX The invention relates to an isolated polypeptide (I), comprising a human
 cleaved collagen triple helix repeat containing 1 (CTHRC1) or an isolated
 mutant CTHRC1 polypeptide (II), comprising substitution of a human CTHRC1
 collagen domain with a mouse collagen 1 alpha 1 collagen domain. (I) and
 (II) are useful for treating or preventing a disease mediated by collagen
 matrix production in a human, which involves administering to a human
 afflicted with the disease an effective amount of CTHRC1, where the
 diseases chosen from fibrosis, constrictive remodeling and restenosis.
 CC (I) or (II) is useful for decreasing levels of bone morphogenetic protein
 CC 1 (BMP1) or BMP1 mRNA in a cell, increasing the level of a propeptide
 CC (chosen from procollagen and a propeptide of lysyl-oxidase) in a cell,
 CC inhibiting collagen formation by a cell, decreasing bone matrix formation
 CC by a cell, decreasing the level of collagen in a cell, increasing the
 CC level of procollagen in a cell, decreasing collagen formation in a mammal
 CC having a condition mediated by collagen formation, where the condition is
 CC chosen from wound scarring, wound healing, keloid formation, inflammation
 CC -associated scarring, pulmonary fibrosis, and angioplasty-associated
 CC vascular fibrosis, or increasing the level of chondrin in a cell, which
 CC involves contacting the cell with (I) or (II). (I) is useful for
 CC inhibiting cross-linking of collagen fibrils in a cell, which involves
 CC contacting a cell with a BMP1 inhibiting amount of (I) or (II), where
 CC BMP1 is responsible for processing a propeptide lysyl-oxidase, and
 CC further where the lysyl-oxidase mediates cross-linking of the collagen
 CC fibrils, thus inhibiting cross-linking of collagen fibrils in the cell.
 CC (I) is useful for treating a disease mediated by expression of BMP1 in a
 CC mammal, increasing the level of bone morphogenetic protein 4 (BMP4) in a
 CC cell, increasing the level of BMP4 promoter activity in a cell, promoting
 CC bone growth in a mammal, promoting differentiation of a stem cell,
 CC decreasing the level of osteopontin (OPN) in a cell, treating a disease
 CC mediated by under expression of BMP4 in a mammal in need, and increasing
 CC the level of a muscle segment homeobox 1 (Meox1) in a cell. The present
 CC sequence represents human CTHRC1, which is used in the exemplification of
 CC the present invention.
 XX SQ Sequence 243 AA;
 Query Match 100.0%; Score 1303; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1e-120;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRPOGPAAASPORLRLGILLLQLPAPSASEBIPKGOKAQLRREVVDLYNGMCLQGPAA 60
 Db 1 MRPOGPAAASPORLRLGILLLQLPAPSASEBIPKGOKAQLRREVVDLYNGMCLQGPAA 60
 Qy 61 GVPGRDGSPGANGIPTGPICPORDGPKGKEGBCLRESSEESWTNYKOCWSSSLNYGIDL 120
 Db 61 GVPGRDGSPGANGIPTGPICPORDGPKGKEGBCLRESSEESWTNYKOCWSSSLNYGIDL 120
 Qy 121 GKIAECKTFKRSNLSALRVFGSLRLKCRNACQWYFTPNAGBCGPPIEAITYLDQ 180
 Db 121 GKIAECKTFKRSNLSALRVFGSLRLKCRNACQWYFTPNAGBCGPPIEAITYLDQ 180
 Qy 181 GSPEMNSTINHRTSSVEGLCGBIGAGLVDAIWGTCSDFPKGDASTGNNSVRIIE 240
 Db 181 GSPEMNSTINHRTSSVEGLCGBIGAGLVDAIWGTCSDFPKGDASTGNNSVRIIE 240
 Qy 241 LPK 243
 Db 241 LPK 243
 RESULT 15
 AEB28819 standard; protein; 243 AA.
 XX AC AEB28819;
 XX DT 08-SEP-2005 (first entry)
 XX Human CTHRC1 protein SEQ ID NO:4.
 XX collagen triple helix repeat containing 1; CTHRC1; vulnerability;
 KW anti-inflammatory; respiratory-gen.; vasoconstrictor; fibrosis;
 KW restenosis;
 KW wound healing; scarring.
 OS Homo sapiens.
 PN US2005147602-A1.
 XX PD 07-JUL-2005.
 XX PP 10-SEP-2004; 2004US-00939233.
 YY

Db 181 GSPEMNSTINHRTSSYEGLCSIGAGIVDVAIWGRCSDYBKGDASTGNNSVSRITEE 240
Qy 241 LPK 243
Db 241 LPK 243

Search completed. April 20, 2006, 09:41:16
Job time : 112.906 secs

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A;Accession: A43903
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'P', 633-1537, 'G' <WES>
A;Cross-references: UNIPARC:UPI0000007C802; GB:S64572; NID:9238616; PIDN:AAB20270.1; PID:R; Venkatesan, M.; De Pablo, F.; Vogeli, G.; Simpson, R.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 3351-3355, 1986
A;Title: Structure and developmentally regulated expression of a Strongylocentrotus purpuratus gene.
A;Reference number: A23940; MUID:86205894; PMID:3458186
A;Accession: A23940
A;Molecule type: DNA
A;Residues: 742-812 <VEN>
A;Cross-references: UNIPARC:UPI00001773DF; EMBL:M13206
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F; 29-161 /Domain: amino-terminal nonhelical, 7S <7SD>
F; 162-1523 /Region: interrupted helical
F; 1524-1754 /Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F; 1534-1634 /Domain: collagen IV carboxyl-terminal repeat <CTN2>
F; 1644-1748 /Domain: collagen IV carboxyl-terminal repeat <CTN2>
F; 129 /Modified site: allyline (Lys) #status predicted

Query Match 9.9% Score 129; DB 2; Length 1752;
Best Local Similarity 22.9%; **Pred.** No. 0.0038;
Matches 47; **Conservative** 20; **Mismatches** 60; **Indels** 78; **Gaps** 9;

Qy 3 PQGPAASPRQRGLLILLLOLPAPSSASEPKGKQAKQLQREPVVDLYNGMCLOGPAGV 62 Db 1453 PQGPPGRDGR-----PGPQS-----PPG----- Qy 63 PGRDGSGANGLPGTGPGRDGFKGFBKGBCURESF-----BBSNT 103 Db 1478 PGVQGNFGVSGVPGFOLKGEGQFRQNGQPDGPDTKBEAGPGSSSSPFITRHSGT 1537	Qy 104 PNYKOC-----SW-----SSLNYGIDLGKTAECTCTFKMRNSNSALRVLFGSRL 147 Db 1538 TSIPQCPQTARMWGHYSLLPVQGNBRGRGDLKGPKGS---LKRFTSMPLFC-NINN 1592	Qy 148 KCRNAACQRWMPFTNGAECSEPLI 172 Db 1593 VCHVASRNDSYWLSTTB---PMPM 1614
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RESULT 3
T20177
hypothetical protein C53B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20177
R;Berks, M.
B;Submitted to the EMBL Data Library, December 1995
A;Reference number: Z19233
A;Accession: T20177
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-89 <WIL>
A;Cross-references: UNIPROT:Q18799; UNIPARC:UPI00000080F8D; EMBL:Z68215; PIDN:CAA92453.1;
A;Experimental source: clone C53B4
A;Genetics:
A;Map position: 4
A;Gene: CESP:C53B4.5
Query Match 9.8% Score 128; DB 2; Length 289;
Best Local Similarity 35.7%; **Pred.** No. 0.00051;
Matches 30; **Conservative** 5; **Mismatches** 19; **Indels** 30; **Gaps** 2;

Qy 25 PAPSSASBIPKGKQKAOLRQREVVDLYNGMCLOGPAGVPGRDGS-----P 69 Db 203 PGPSSGCGPQPGPQGS-----RGPGQPGCGDKAQGCGPGEKGANGEPGPQGP 247
--

Query Match 70 GANGIPTPGIFGRDGFKGEKGBC 93
Db 248 GRDGQGPQPGQFGRDHGPGEKGVC 271

- | |
|--|
| A; Cross-references: UNIPARC:UPI0000173BAA; GB:K01228; NID:9180391; PMID:AA51995_1; PID:R; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F. |
| A; Title: A base substitution in the exon of a collagen gene causes alternative splicing |
| R; Biochemistry 9, 4699-4706, 1970 |
| A; Title: Isolation and characterization of the cyanogen bromide peptides from the alpha 1(I) chain of collagen alpha 1(S)1 isolated from bone after pepsin digestion |
| A; Reference number: S09400; MUID:89356643; PMID:2767050 |
| A; Accession: S09400 |
| A; Molecule type: mRNA |
| A; Residues: 156-183 <WET> |
| A; Cross-references: UNIPARC:UPI0000173B3E |
| A; Experimental source: skin |
| A; Evidence for 170-allysine |
| R; Baetge, B.M.; Bornstein, P. |
| A; Cross-references: UNIPARC:UPI0000173B3F |
| A; Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z' |
| A; Accession: B90567 |
| A; Molecule type: protein |
| A; Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z' |
| A; Cross-references: UNIPARC:UPI0000173B3F |
| A; Experimental source: skin |
| A; Evidence for 170-allysine |
| R; Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutmann, R.; Mueller, F |
| Eur. J. Biochem. 192, 153-159, 1990 |
| A; Title: A critical crosslink in human-bone-derived collagen type I. Specific cleavage of the alpha 1(I) propeptide at residue 199 |
| A; Reference number: S11372; MUID:90382436; PMID:2169412 |
| A; Accession: S11372 |
| A; Molecule type: protein |
| A; Residues: 173-187/274-287, 'P', 289 <BAE> |
| A; Cross-references: UNIPARC:UPI0000173B41 |
| A; Note: Sequence of collagen alpha 1(S)1 isolated from bone after pepsin digestion |
| R; Deak, S.B.; Schoiz, P.M.; Amenta, P.S.; Constantino, C.D.; Levi-Minzi, S.A.; Gonzalez |
| J. Biol. Chem. 266, 21827-21832, 1991 |
| A; Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain cooperative melting of intact type I collagen |
| A; Reference number: 155342; MUID:92042022; PMID:1718984 |
| A; Accession: 155342 |
| A; Status: translated from GB/BMBL/DBJ |
| A; Molecule type: mRNA |
| A; Residues: 258-268/1347-1357 <DEA> |
| A; Cross-references: UNIPARC:UPI0000173B42; UNIPARC:UPI0000173B43; GB:S67495; NID:9239007 |
| A; Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report |
| R; Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W. |
| Matrix 10, 124-130, 1990 |
| A; Title: Segmental amplification of the entire helical and telopeptide regions of the cDNA |
| A; Reference number: 152905; MUID:90326017; PMID:2374517 |
| A; Accession: S15989 |
| A; Molecule type: protein |
| A; Cross-references: UNIPARC:UPI000014DF11 |
| A; Experimental source: skin |
| A; Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine |
| R; Labhard, M.E.; Hollister, D.W. |
| Connect. Tissue Res. 29, 1-11, 1993 |
| A; Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of collagen |
| A; Reference number: 152905; MUID:93339042; PMID:83139541 |
| A; Status: translated from GB/BMBL/DBJ |
| A; Molecule type: mRNA |
| A; Residues: 281-302/402-420; 823-843; 925-944 <LAB> |
| A; Cross-references: UNIPARC:UPI0000173B44; UNIPARC:UPI0000173B45; UNIPARC:UPI0000173B46; |
| A; Note: mutant sequence from patient with osteogenesis imperfecta |
| R; Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J. |
| J. Biol. Chem. 263, 5213-5223, 1988 |
| A; Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha 1(I) and proalpha 2(I) chains of type I collagen |
| A; Reference number: A90476; MUID:84080305; PMID:66889127 |
| A; Accession: A90476 |
| A; Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER> |
| A; Cross-references: UNIPARC:UPI0000173BAA; GB:K01228; NID:9179612; PMID:917961 |
| A; Note: sequence partially completed for missing nucleotides by A29439 |
| R; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F. |
| J. Biol. Chem. 260, 691-694, 1985 |
| A; Title: Multixon deletion in an osteogenesis imperfecta variant with increased type I collagen synthesis |
| A; Reference number: A22151; MUID:85104934; PMID:2281843 |
| A; Accession: A22161 |
| A; Molecule type: DNA |
| A; Residues: 47-594 'R', 596-607 <CH3> |
| A; Cross-references: UNIPARC:UPI000011P796; GB:K03178; GB:K03179; NID:9179612; PMID:917961 |
| A; Note: the authors translated the codon CGT for residue 595 as pro |
| R; Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H. |
| Am. J. Hum. Genet. 46, 1034-1040, 1990 |
| A; Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained by a deletion in the 5' flanking region of the collagen type I gene |
| A; Reference number: A35336; MUID:90252792; PMID:2339700 |
| A; Molecule type: mRNA |
| A; Residues: 710-720, 'E', 722-727, 'E', 739-745 <WAL> |
| A; Cross-references: UNIPARC:UPI0000173B43 |
| A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu |
| R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cettori, G.; Brunelli, P.C.; Motte: Hum. Mol. Genet. 3, 2201-2206, 1994 |
| A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the alpha 1(I) chain of collagen |
| A; Reference number: 154365; MUID:95187161; PMID:7881420 |
| A; Molecule type: DNA |
| A; Status: translated from GB/EMBL/DBJ |
| A; Residues: 746-766 'S', 768-781 <FOR> |
| A; Cross-references: UNIPARC:UPI00001646FA; GB:L47667; NID:9109093; PMID:AB59576_1; PMID:R; Chessier, S.D.; Wallis, G.A.; Byers, P.H. |
| A; Note: sequence extracted from NCBI backbone (NCBIN:136441, NCBI:133645) |
| J. Biol. Chem. 268, 18218-18225, 1993 |
| A; Title: Mutation in the carboxy-terminal propeptide of the pro alpha 1(I) chain of type I collagen |
| A; Reference number: A47426; MUID:93352646; PMID:8349697 |
| A; Molecule type: mRNA |
| A; Residues: 1179-1216, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE> |
| A; Cross-references: UNIPARC:UPI0000073A2A; GB:S6596; PMID:9407589; PMID:AB27856_1; PMID:R; Cohn, D.H.; Apone, S.; Byre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nic |
| A; Note: sequence extracted from NCBI backbone (NCBIN:136441, NCBI:133645) |
| J. Biol. Chem. 263, 14605-14607, 1988 |
| A; Title: Normal dermal fibroblast culture |
| A; Cross-references: UNIPARC:UPI0000173B4C |
| A; Experimental source: normal dermal fibroblast culture |
| A; Molecule type: mRNA |
| A; Residues: 1179-1464 <CH4> |
| A; Cross-references: UNIPARC:UPI0000173B4C |
| A; Experimental source: fetal cell |
| A; Molecule type: mRNA |
| A; Residues: 1179-1316, 1339-1464 <CH6> |
| A; Cross-references: UNIPARC:UPI0000173B4E |
| A; Experimental source: fetal cell |
| A; Molecule type: mRNA |
| A; Residues: 1179-1216, 'H', 1278-1464 <CH5> |
| A; Cross-references: UNIPARC:UPI0000173B4D |
| A; Experimental source: fetal cell |
| A; Molecule type: mRNA |
| A; Residues: 1179-1387, 'R', 1389-1464 <CH7> |
| A; Cross-references: UNIPARC:UPI0000173B4F |
| A; Experimental source: fetal cell 88-251 |
| R; Cohn, D.H.; Apone, S.; Byre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nic |
| J. Biol. Chem. 263, 14605-14607, 1988 |
| Query Match 9 / 8%; Score 127.5; DB 1; Length 1464; |
| Best Local Similarity 37.4%; Pred. No. 0.0041; 2; Mismatches 22; Indels 33; Gaps 4; |
| Matches 34; Conservative 34; |
| Qy 3 PQGPAS -PORIGGLLILLIQLPAPSSASEIPKGKQAKLROREVVDLYNGMCLQGPA 60 |
| Db 357 PQGPSEGPGV93 -----EPSPG-----PAG-----AAGPA 385 |
| Qy 61 GVPGRGSPGANGLPTPGFGRGFKGKG 91 |

Db 386 GNPAGDQPGKANGAPGIAGAPGFFGARG 416

C;Accession: S28791
R;Nah, H.D.; Barembaum, M.; Upholt, W.B.RESULT 5
T29031 hypothetical protein F53G12.7 - Caenorhabditis elegansC;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004C;Accession: T29031
R;Wu, X.; Graves, T.

A;Cross-references: UNIPROT:001799; UNIPARC:UPI0000078FFF; EMBL:AF003139; PIDN:AAB54156.

A;Experimental source: strain Bristol N2; clone F53G12

C;Genetics:
A;Gene: CESP:F53G12.7A;Map position: 1
A;Introns: 59/3; 138/1; 223/2

Query Match 9.7%; Score 126; DB 2; Length 327;

Best Local Similarity 34.4%; Pred. No. 0.0011;
Matches 32; Conservative 21; Indels 38; Gaps 3;Qy 1 MRPOGPAASPQRLRGILLLLLQLPAPSASEIPIKGKQKAQLRQREVVDLYNGMCLOQPA 60
Db 2611 MGQPQP-----PGRGP-----PRGDGA-----GGEK 282C;Accession: A5267
R;Zhang, K.; Thorner, P.S.; Marrano, P.; Baumal, R.; McInnes, R.R.

C;Cross-references: UNIPROT:Q28247; UNIPARC:UPI0000126D56; GB:U07888B; PMID:9469547; PIDN:

A;Title: Canine x chromosome linked hereditary nephritis: a genetic model for human X-11

A;Type IV.

A;Reference number: A55267; MUID:94224868; PMID:8171024

A;Accession: A5267
A;Status: preliminaryA;Molecule type: mRNA
A;Residues: 1-754 <ZIE>

A;Cross-references: UNIPROT:Q28247; UNIPARC:UPI0000126D56; GB:U07888B; PMID:9469547; PIDN:

C;Superfamily: collagen alpha 1(IV) chain

Query Match 9.7%; Score 126; DB 2; Length 754;

Best Local Similarity 35.4%; Pred. No. 0.0027;
Matches 34; Conservative 7; Indels 22; Gaps 4;Qy 3 PQQGPAASPQRLRGILLLLLQLPAPSASEIPIKGKQ-KAQLRQREVVDLYNGMC 55
Db 332 PQGPPERP-----GLPGEPGRGLPGNGKIGERGNPGQGPGLKGKD-- 377C;Accession: A5267
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Saus, J.

A;Cross-references: UNIPROT:1P0796; UNIPARC:UPI000016A42D; GB:M92993; PID:9177895; PIDN:AAA21610.1; PID:

A;Note: sequence extracted from NCBI Backbone (NCBIP:115597)

R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Saus, J.

J. Biol. Chem., 269, 17358, 1994

A;Reference number: A44043; MUID:93015626; PMID:1400291

A;Accession: A44043
A;Molecule type: DNA; mRNA
A;Residues: 1386-1670 <QD1>

A;Cross-references: UNIPARC:UPI000016A42D; GB:M92993; PID:9177895; PIDN:AAA21610.1; PID:

A;Note: sequence extracted from NCBI Backbone (NCBIP:115597)

R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Saus, J.

J. Biol. Chem., 268, 11090-11294, 1993

A;Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.

A;Reference number: A45971; MUID:3328084; PMID:9505332

A;Accession: A45971
A;Status: nucleic acid sequence not shownA;Molecule type: mRNA
A;Residues: 1427-1444 <BER>RESULT 7
S28791 collagen alpha 1(XI) chain - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

- | | |
|---|--|
| A; Cross-references: UNIPARC:UPI0000173B85 | |
| A; Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly identified | |
| R; Morrison, K.E.; Miyayama, M.; Yang, Feng, T.L.; Reeder, S.T. | |
| Am. J. Hum. Genet. 49, 545-554, 1991 | |
| A; Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of collagen alpha1 (III) chain of human type-III procollagen gene | |
| A; Reference number: S04642; PMID:89350838; MUID:2764886 | |
| A; Accession: S04642 | |
| A; Molecule type: mRNA | |
| A; Residues: 1-196 <B85> | |
| A; Cross-references: UNIPARC:UPI0000173B80; EMBL:X14420; PIDN:CAA32583.1; PI: R; Benson, C.V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F. | |
| A; Note: the complete sequence is not shown | |
| Gene 78, 255-265, 1989 | |
| A; Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene | |
| A; Reference number: PE0011; MUID:89378752; PMID:2770833 | |
| A; Accession: PE0011 | |
| A; Molecule type: DNA | |
| A; Residues: 1-176 <B85> | |
| A; Cross-references: UNIPARC:UPI000016A703; GB:M26939; NID:9180813; PIDN:AAA52040.1; PID: R; Tomar, P.D.; Ricca, G.A.; de Crombrugge, B. | |
| A; Note: the authors translated the codon CAG for residue 154 as His | |
| R; Janecko, R.A.; Ramirez, F. | |
| A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human proalpha1 (III) collagen | |
| A; Reference number: S01726; MUID:88303360; PMID:3405773 | |
| A; Accession: S01726 | |
| A; Molecule type: mRNA | |
| A; Residues: 1-170 <TOM> | |
| A; Cross-references: UNIPARC:UPI000016A706; EMBL:X07240; PIDN:930060; PID: R; Tomar, P.D.; Ricca, G.A.; de Crombrugge, B. | |
| A; Note: the authors translated the codon CAG for residue 154 as His | |
| R; Janecko, R.A.; Ramirez, F. | |
| A; Title: Nucleotide and amino acid sequences of the entire human alpha1 (III) collagen | |
| A; Reference number: S04887; MUID:89386015; PMID:2780304 | |
| A; Accession: S04887 | |
| A; Molecule type: mRNA | |
| A; Residues: 149-163 <G>; 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634 <TOM> | |
| A; Cross-references: UNIPARC:UPI000016A61C; EMBL:X53332; PIDN:229545; PID: R; Seyer, J.M.; Kang, A.H. | |
| A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide sequence of collagen: amino acid sequence of cyanogen bromide peptide. | |
| A; Reference number: A90399; MUID:77134724; PMID:557335 | |
| A; Accession: A90399 | |
| A; Molecule type: protein | |
| A; Residues: V, 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEY1> | |
| A; Cross-references: UNIPARC:UPI0000173B81 | |
| A; Experimental source: liver | |
| A; Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to the Asn 154 residue | |
| A; Accession: 151868; MUID:93304430; PMID:8317500 | |
| A; Accession: 151868 | |
| A; Status: preliminary; translated from GB/EMBL/DDBJ | |
| A; Molecule type: protein | |
| A; Residues: V, 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY1> | |
| A; Cross-references: UNIPARC:UPI000000014; GB:S62925; NID:9386425; PIDN:AADI3937.1; PID: R; Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H. | |
| A; Note: author submitted corrections to A90399 | |
| A; Experimental source: liver | |
| A; Title: Abnormal type III collagen produced by an exon-17 skipping mutation of the COL3A1 gene | |
| A; Reference number: S59511; MUID:96067614; PMID:7487954 | |
| A; Accession: S59511 | |
| A; Molecule type: mRNA | |
| A; Residues: 302-433 <CHI> | |
| A; Cross-references: UNIPROT:PO461; UNIPARC:UPI0000000CDE; EMBL:X14420; PIDN:930057; PID: S719877; GB:S719877; PIDN:91195576; PIDN:91195576 | |
| A; Cross-references: UNIPROT:PO461; UNIPARC:UPI0000000CDE; EMBL:X14420; PIDN:930057; PID: S719877; GB:S719877; PIDN:91195576; PIDN:91195576 | |

R;Seyer, J.M.; Kang, A.H. Biochemistry 17, 3404-3411, 1978 A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CbR peptide residues: 159025; NUID:159025; PMID:687591	A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm of chromosome 17, 3404-3411, 1978 A;Reference number: 159025; NUID:159025; PMID:687591 A;Accession: I79359 A;Status: translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Residues: 1165-1196 <EMA> A;Cross-references: UNIPARC:UPI000016AB66; GB:MI1134; NID:9180417; PID:AAA52004.1; PID:R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F. J.Biol.Chem. 260, 4357-4363, 1985 A;Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen. Part A;Reference number: A92516; NUID:915700; PMID:2579949 A;Accession: A92516 A;Molecule type: DNA A;Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU> A;Cross-references: UNIPARC:UPI000173B89; GB:MI0615; GB:MI0793; GB:MI0795; G;A;Experimental source: liver A;Note: the authors translated the codon RTC for residue 1057 as Tyr; the codons given for position +5 of the lysines are 5-hydroxylated and some are subsequently O-3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O-3-hydroxylated. C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit of type III collagen are a homotrimer of monomers initially linked by disulfide bonds. The length of the polymer is determined by the length of the repeating unit. C;Function: C;Description: structural component of extracellular fibrous polymer that maintains integrity of the extracellular matrix. C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxy1-terminal homology; C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydroxyproline; signal sequence #status predicted <SIG> F;1-23/Domain: amino-terminal propeptide #status predicted <PRO> F;24-153/Domain: carboxyl-terminal propeptide #status predicted <PRO> F;122-146/Domain: carboxyl-terminal homology #status predicted <CP> F;1228-1446/Domain: fibrillar collagen carboxyl-terminal homology #status predicted <FC>> F;24/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted <MAT> F;154-167/Region: collagen alpha 1(III) chain #status predicted <MAT> F;154/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted <MAT> F;168-1196/Region: helical attachment (R-G-D) motif F;1091-1093/Region: helical attachment (R-G-D) motif F;1119-122/Region: carboxyl-terminal telopeptide A;Cross-references: UNIPARC:UPI00000004A1; GB:J05617; GB:MS55603; GB:9180878; A;Accession: S02119 A;Status: translation not shown A;Molecule type: mRNA A;Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN> A;Cross-references: UNIPARC:UPI0000173B86; EMBL:X06700; NID:930053; PID:CAA29886.1; PID:R;Seyer, J.M.; Kang, A.H. Biochemistry 20, 2621-2627, 1981 A;Title: Covalent structure of collagen: amino acid sequence of alpha 1(III)-CB9 from type III collagen. Part A;Reference number: 81208139; PMID:7016180 A;Accession: A90446 A;Molecule type: protein A;Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-1161 <EMA> A;Cross-references: UNIPARC:UPI0000173B87 A;Experimental source: liver R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenblum, J.; Myers, Nucleic Acids Res. 12, 9333-9394, 1984 A;Title: Molecular cloning and carbohydrate analysis of human type III procollagen A;Reference number: A93551; PMID:8508794; PMID:6096827 A;Accession: A93551 A;Molecule type: mRNA A;Residues: 1065-1155, 'P', 1157-1466 <LOI> A;Cross-references: UNIPARC:UPI0000173B88; EMBL:X01655; PID:929584; PID:CA;R;Mishklish, M.; Dalglish, R.; Klueve-Becherman, B.; Renard, S.I.; Tolstoichev, P.; Brant, Biochemistry 25, 1408-1413, 1986 A;Title: Human type III collagen gene expression is coordinately modulated with the type III collagen gene. Part A;Reference number: 152393; PMID:86187804; PMID:3754462 A;Accession: 152393 A;Status: translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Residues: 1161-1200 <MISS> A;Cross-references: UNIPARC:UPI000016AB5; GB:MI1346; NID:9180415; PID:AAA52003.1; PID:R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C. Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
	RESULT 10 S16366 Collagen alpha 2(IV) chain precursor - pig roundworm C;Species: Ascaris suum (pig roundworm) C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 C;Accession: S16366 R;Pettit, J.; Kingston, J.B. J.Biol.Chem. 266, 16149-16156, 1991 A;Title: The complete primary structure of a nematode alpha-2(IV) collagen and the part A;Reference number: S16366; PMID:91340768; PMID:1714907 A;Molecule type: mRNA A;Residues: 1-1763 <JBIG>
	Query Match Score 124; DB 1; Length 1466; Best Local Similarity 37.0%; Pred. No. 0.008; Matches 46; Deletions 14; Gaps 5; Matches 40; Conservative 8; Mismatches 46;
	Qy 22 LQLPAAASSAASPIKPGKQKAQLQRREVVLY--NGMCLOGPAGVGPGRDGSPPANGIFGTG 79 Db 72 LDCPNP---EIPPFECACCVAQPQPPTAPTRPPNGQQGPOGKFGDPGPPIPGRNGDGP 127
	Qy 80 IPGRDGFKGERGECEHESF---EESMTPNXQCSSSLNNGIDLGKIA 124 Db 128 QFGSPGSPGPGIC--ESCPTEGPQNTYSQYSDVKS--GVAVGSLA 170

A; Cross-references: UNIPROT:P27393; UNIPARC:UPI0000126D40; GB|M67507; NID:9159649; PIDN: T26185
 C; Genetics: 229/3; 266/3; 305/3; 360/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1;
 C; Intron: Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C; Accession: T26185
 R; Gardner, A.
 Submitted to the EMBL Data Library, October 1996
 A; Reference number: 220166
 A; Accession: T26185
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-304 <WIL>
 A; Cross-references: UNIPROT:Q9U349; UNIPARC:UPI000007B910; EMBL:Z81138; PIDN:CAB03475.1
 A; Experimental source: clone W05B2
 C; Genetics:
 A; Gene: CBSP:W05B2.1
 A; Map position: 3
 A; Introns: 27/3

Query Match 9.5%; Score 124; DB 2; Length 1763;
 Best Local Similarity 25.8%; Pred. No. 0.011; Gaps 16;
 Matches 67; Conservative 24; Mismatches 93; Indels 76; Gaps 16;

Qy	5	GPGRSPQRGLLILLLQ-LPAPSSAIIPKGKQAKLQRQREVVDLNLNGM-CLGQAGV	62
Db	1449	GPMCAPI-GIRGEKGIPGLDGLPGPSGS-----PPFGAGAGR-----DGPQGPMPGKERA	1498
Qy	63	PGRDGSPGANGIPTGPGLGRDGFKGKBECLRESPF--EESWTPNPKQS-----W-	111
Db	1499	PGLDGPFGTEGIPPTGPGLGPSPKGPKDFLYKHSOTSEVQCPPOVKWDG	1558
Qy	112	-----SSLNYGIDLIGKIAETCFPTKMRNSNALSRLVSGSLRLKCRNAC-----QCR	156
Db	1559	YSLIYBNEKSNQDGLHAGSC----LSRFSTMPN-----CDVNVCNTYASRNDSY	1609
Qy	157	WFTFNGACSGKPLIENIYLQGSPMNSTINHRSSVBLCEGGAGLVDV--AI	213
Db	1610	WLST-----TAPPPMMPV-----SEGGIEPTISRCAVCEA-PANVIAVHSQTI	1651
Qy	214	WVGTCSDYLPKGDASTGNNSV	233
Db	1652	QIPNCNP-----GMNSL	1663

RESULT 13
 T26184
 hypothetical protein W05B2.6 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C; Accession: T26184
 R; Gardner, A.
 Submitted to the EMBL Data Library, October 1996
 A; Reference number: 220166
 A; Accession: T26184
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-304 <WIL>
 A; Cross-references: UNIPROT:Q9XVG3; UNIPARC:UPI0000079930; EMBL:Z81138; PIDN:CAB03474.1
 A; Experimental source: clone W05B2
 C; Genetics:
 A; Gene: CBSP:W05B2.6
 A; Map position: 3
 A; Introns: 27/3

Query Match 9.4%; Score 123; DB 2; Length 304;
 Best Local Similarity 33.0%; Pred. No. 0.0018; Gaps 2;
 Matches 30; Conservative 5; Mismatches 24; Indels 32; Gaps 2;

Qy	3	PGPAAASPQRGLLILLLQLPAPSSAIIPKGKQAKLQRQREVVDLNLNGM-CLGQAGV	62
Db	227	PGPSP-----PGPAGSPGAPGPGQAOG-----APGPKGP	254
Qy	63	PGRDGSPGANGIPTGPGLGRDGFKGKBECLRESPF--EESWTPNPKQS-----W-	111
Db	255	SGRPQGPAGDNPGAPGQSGGAGKGIC	285

RESULT 14
 S22917
 collagen alpha 5(IV) chain precursor, renal splice form - human
 N; Alternate names: procollagen alpha 5 (IV) chain
 N; Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
 C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C; Accession: S22917; A54365; A37079; A37122; 154317; A34850; S18850; 156971; 176598; A35

Query Match 9.5%; Score 123.5; DB 2; Length 311;
 Best Local Similarity 53.3%; Pred. No. 0.0017; Gaps 1;
 Matches 24; Conservative 4; Mismatches 12; Indels 5; Gaps 1;

Qy	53	GMC-----LOGPACVPGRDGSPGANGIPTGPGLGRDGFKGKGE	92
Db	227	GRKDEVNVAQGPSPGSPGFPGLPQDPGLPQDPGNPQDQBGPAGE	271

RESULT 12
 S22917

R; Zhou, J.; Hertz, J.M.; Leinonen, A.; Tryggvason, K.
 J. Biol. Chem. 267, 12475-12481, 1992
 A; Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and identification of the gene to the regi-
 n. Alport syndrome patient.
 A; Reference number: S22917; MUID:92316923; PMID:1352287
 A; Accession: S22917
 A; Molecule type: mRNA
 A; Residues: 1-967 <ZINC>
 A; Cross-references: UNIPROT:P29400; UNIPARC:UPI0000173BDF; GB:M90464; PID:9180826; PMID:
 R; Zhou, J.; Leinonen, A.; Tryggvason, K.
 J. Biol. Chem. 269, 6608-6614, 1994
 A; Title: Structure of the human type IV collagen COL4A5 gene.
 A; Reference number: A54365; MUID:94165049; PMID:8120014
 A; Accession: A54365
 A; Molecule type: DNA
 A; Residues: 1-922 <ZINC>
 A; Cross-references: UNIPARC:UPI0000173BEO; GB:U04470; NID:9463378; GB:U04520; NID:946342
 R; Zhou, J.; Mochiuki, T.; Smets, H.; Antignac, C.; Laurila, P.; de Paep, A.; Tryggvason, K.;
 Science 261, 1167-1169, 1993
 A; Title: Deletion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited SM
 A; Reference number: A57073; MUID:9361972; PMID:8556449
 A; Accession: A57079
 A; Molecule type: DNA
 A; Residues: 1-27 <ZINC>
 A; Cross-references: UNIPARC:UPI000007378A; GB:237153; NID:9587203; PID:CAA85512.1; PID:
 R; Pihalajaniemi, T.; Pihlajaniemi, E.R.; Myers, J.C.
 J. Biol. Chem. 265, 13758-13766, 1990
 A; Title: Complete primary structure of the triple-helical region and the carboxyl-terminal
 A; Accession: A37122
 A; Molecule type: mRNA
 A; Residues: 84-439, 'GS', 442-624, 'LALQ', 629-666, 'FR', 669-887, 'R', 889-1264, 1271-1691 <PIH>
 A; Cross-references: UNIPARC:UPI0000173BEE; GB:J05558; EMBL:M58226; NID:91314209
 A; Note: submitted to the EMBL Data Library, 1991
 R; Renieri, A.; Seri, M.; Myers, J.C.; Pihalajaniemi, T.; Massella, L.; Rizzoni, G.; De Ma-
 Hum. Mol. Genet. 1, 127-129, 1992
 A; Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid in
 A; Reference number: 154317; MUID:93244772; PMID:1363780
 A; Accession: 154317
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 313-324, 'E', 326-330 <REN>
 A; Cross-references: UNIPARC:UPI000016B3D0; GB:MS9334; NID:9299946; PID:AAA52045.1; PID:
 R; Hoibikka, S.L.; Bddy, R.L.; Byers, M.G.; Hoeijmakers, M.; Shows, T.B.; Tryggvason, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990
 A; Title: Identification of a distinct type IV collagen alpha chain with restricted kidney
 A; Reference number: A34850; MUID:91169491; PMID:90160375; PMID:1689491
 A; Accession: A34850
 A; Molecule type: mRNA
 A; Residues: 914-1264, 1271-1691 <HOS>
 A; Cross-references: UNIPARC:UPI000016A70B; EMBL:M31115; NID:9180824; PID:AAA52045.1; PI
 R; Zhou, J.; Hostrikka, S.L.; Chow, L.T.; Tryggvason, K.
 Genomics 9, 1-9, 1991
 A; Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene that
 A; Reference number: A37969; MUID:91169491; PMID:2004755
 A; Accession: S18850
 A; Molecule type: DNA
 A; Residues: 924-1264, 1271-1691 <ZH3>
 A; Cross-references: UNIPARC:UPI000016A437; EMBL:M63456; EMBL:M63457; EMBL:M63467; EMBL:M63468; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:917792
 R; Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Berghe, H.; Cassiman, J.J.; N-
 Kidney Int. 44, 1316-1321, 1993
 A; Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a complex
 A; Reference number: 156971; MUID:94133540; PMID:8301933
 A; Accession: 156971
 A; Molecule type: mRNA
 A; Residues: 1255-1276 <GH01>
 A; Cross-references: UNIPARC:UPI000016B421; GB:S69168; NID:9545095; PID:AAAC60612.1; PID:
 A; Note: kidney splice form
 A; Accession: I76598
 A; Status: translated from GB/EMBL/DBJ

A; Molecule type: mRNA
 A; Residues: 1264-1291, 'TFLGYLACLV' <GU02>
 A; Cross-references: UNIPARC:UPI000011D0FD; GB:S69169; NID:9545097; PID:
 A; Note: frameshift mutation in patient with Alport syndrome
 R; Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, A.S.; Goddard, A.D.; Shear, D.; So
 Am. J. Hum. Genet. 46, 1024-1033, 1990
 A; Title: Molecular cloning of alphas(IV) collagen and assignment of the gene to the regi-
 A; Reference number: A35335; MUID:2025291; PMID:1339699
 A; Accession: A35335
 A; Status: nucleic acid sequence not shown
 A; Molecule type: mRNA
 A; Residues: 1448-1477 <MYB>
 A; Cross-references: UNIPARC:UPI0000173BE2
 R; Nakazato, H.; Hattori, S.; Ushijima, T.; Matsura, T.; Koitabashi, Y.; Takada, T.; Yoshi-
 Kidney Int. 46, 1307-1314, 1994
 A; Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in primord-
 A; Reference number: 156975; MUID:95156893; PMID:7853788
 A; Status: translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1555-1562 <NRK>
 A; Cross-references: UNIPARC:UPI00000001F8; GB:S75503; PID:9013882; PID:AA33374.1; PID:
 A; Note: permanent termination mutation from a patient with Alport syndrome; one other mu-
 R; Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Tryggvason, K.;
 Genomics 17, 485-489, 1993
 A; Title: Identification of four novel mutations in the COL4A5 gene of patients with Alpo-
 A; Reference number: 154188; MUID:94010348; PMID:8406498
 A; Accession: 154188
 A; Status: translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 164-1607, 'VHDAYKC' <LEM>
 A; Cross-references: UNIPARC:UPI000011F85C; GB:S65767; NID:9425563; PID:AA139957.1; PID:
 A; Note: frameshift mutation from a patient with Alport syndrome; five other mutations at
 C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C)
 ed and subsequently O-Glycosylated.
 A; Gene: GDB:COL4A5; ATS
 A; Cross-references: GDB:120596; OMIM:303630
 A; Map Position: Xq22-Xq22
 A; Introns: 27/3; 4/7/3; 77/3; 92/3; 107/3; 128/3; 146/3; 155/3; 182/3; 215/3; 229/3;
 A; Domain: signal sequence #status predicted <SIG>
 F; 27-1691/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <MAT1>
 A; Note: the alpha 5(IV) and alpha 6(IV) chain genes are encoded on opposite strands with
 C; Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 5(IV)
 monomer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a-
 mer associations in the interrupted helical domain (with disulfide and desmosine cross-link-
 C; Function: C; Superfamily: collagen alpha 1(IV) chain
 C; Superfamily: collagen alpha 1(IV) chain
 C; Keywords: Alport syndrome; basement membrane; coiled coil; extracellular basement membrane
 C; Description: minor structural component of extracellular basement membrane
 C; Superfamily: collagen alpha 5(IV) chain
 F; 27-1691/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <SIG>
 F; 27-1264,1271-1691/Product: collagen alpha 5(IV) chain, leukocyte splice form #status predicted
 F; 27-41/Domain: amino-terminal nonhelical, NC2 #status predicted <NC2>
 F; 42-1462/Region: interrupted helical
 F; 1463-1691/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NC1>
 F; 1473-1573/Domain: collagen IV carboxyl-terminal repeat <CT1>
 F; 1583-1687/Domain: collagen IV carboxyl-terminal repeat <CT2>
 F; 29-32,33,40,124,451,484/Disulfide bonds: interchain #status predicted
 F; 1255/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 1452-1570,1515-1573/Disulfide bonds: (or 1482-1573, 1515-1570) #status predicted
 F; 1527-1533,1638-1644/Disulfide bonds: #status predicted (or 1592-1687, 1626-1684) #status predicted
 F; 1592-1684,1626-1687/Disulfide bonds:
 Query Match 9 4%; Score 123; DB 1; Length 1691;
 Best Local Similarity 36 5%; Pred. No. 0 0.13333; Indels 16; Gaps 4;
 Matches 35; Conservative 7; Mismatches 38;
 Qy 3 PQGPAA--SPORLGRULLLUQLPAPSSASBIP----KSKKQKAQLQRREVVDLYNGMC 55
 Db 1256 PQGPGRPGPTGFGQ-----LGPPEGPGLPQGPGQPLPGPGLKG 1306
 Qy 56 LQGPAGVPGRDGSPGANGIPTGPGLPQGPKGEGKG 91

Db 1307 DQGPGLQGNGPGRGLNNGMKGDPLPGVPGFPGMKG 1342

RESULT 15
T24482
hypothetical protein T05A1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24482
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Accession: T24482
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-300 <WIL>
A;Cross-references: UNIPROT:Q22183; UNIPARC:UPI00000765DA; EMBL:Z68219; PIDN:CAA92476.1;
A;Experimental source: Clone T05A1
C;Genetics:
A;Gene: CESP:T05A1.2
A;Map position: 4
A;Introns: 7/3

Query Match 9.4%; Score 122.5; DB 2; Length 300;
Best Local Similarity 31.5%; Prod. No. 0.002;
Matches 35; Conservative 11; Mismatches 28; Indels 37; Gaps 5;
Matches 35; Conservative 11; Mismatches 28; Indels 37; Gaps 5;

Qy 3 PQQPAASQR--LRGLLILQLQLPAPSASEIPKGKQKAQURQREYVDLYNGMCLQGP- 59
Db 189 PPGPNGHGPKGSQG-----PPGPQHSDEPKPCQPGQGRAGB-----RGPR 231

Qy 60 --AGVPGRDGSPSA-----NGIPTGTPGIPGRDGFKGKEKGC 93
Db 232 GVAIGKGRDGAPSPGQGPGRGGPBPQDGAPGQPGTPGSDGTGPKGIC 282

Search completed: April 20, 2006, 09:50:28
Job time : 21.6941 secs

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Scoring table:	BLOSUM62					
Gapop:	10.0 , Gapext 0.5					
Searched:	2166443 seqs, 70528306 residues					
Total number of hits satisfying chosen parameters:	2166443					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0% Maximum Match 100%					
Database :	UniProt_05_80: 1: uniprot_sprot: 2: uniprot_trembl: * Listing First 45 summaries					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES	*					
Result No.	Score	Query	Match	Length	DB ID	Description
1	1303	100.0	243	1	CTHR1_HUMAN	Q96cg8 homo sapien
2	1225	94.0	245	1	CTHR1_RAT	Q8cg08 rattus norv
3	1210	92.9	245	1	CTHR1_MOUSE	Q9d1d6 mus musculu
4	992	76.1	258	2	Q5H2D2_XENTR	Q5hd2 xenopus tro
5	951	73.0	191	2	Q4SMQ6_TETNG	Q4smq6 tetraodon n
6	928	71.2	231	2	Q6AXL0_BRARE	Q6axl0 brachydario
7	139	10.7	565	2	Q8K036_MOUSE	Q8k036 mus musculu
8	135	10.4	1208	2	Q4RX03_TETNG	Q4rx03 tetraodon n
9	133.5	10.2	652	2	Q5PAT5_HUMAN	Q5ats5 homo sapien
10	133.5	10.2	683	2	Q5TAT4_HUMAN	Q5tat4 homo sapien
11	133.5	10.2	717	2	Q9N052_HUMAN	Q9nq52 homo sapien
12	133.5	10.2	717	2	Q5PAT6_HUMAN	Q5tat6 homo sapien
13	133	10.2	289	2	Q6IBS4_CELBR	Q6ibs4 caenorhabdi
14	131.5	10.1	246	1	C1OC_MOUSE	Q02105 mus musculu
15	131.5	10.1	1472	2	Q90DA0_CHICK	Q90za0 gallus gall
16	130.5	10.0	705	2	Q4S2U5_TETNG	Q4s2u5 tetraodon n
17	129	9.9	287	2	Q8CFR0_MOUSE	Q8cfro mus musculu
18	129	9.9	1752	2	Q07265_STRPU	Q07265 stronglyloce
19	128	9.8	289	2	Q18199_CAEEL	Q18199 caenorhabdi
20	128	9.8	1333	2	Q4SK58_TETNG	Q4sk58 tetraodon n
21	127.5	9.8	289	2	Q6QOP0_CELBR	Q6qop0 caenorhabdi
22	127.5	9.8	358	2	Q6MYY7_PARW	Q6mey7 paracitamol
23	127.5	9.8	1069	2	Q6LAN8_HUMAN	Q6lan8 homo sapien
24	127.5	9.8	1461	2	Q76045_HUMAN	Q76045 homo sapien
25	127.5	9.8	1464	1	COL1_HUMAN	P02452 homo sapien
26	127.5	9.8	1464	2	Q8N473_HUMAN	Q8n473 homo sapien
27	127.5	9.8	1467	2	Q59864_HUMAN	Q59f64 homo sapien
28	127	9.7	291	2	Q9NAR3_CAEEL	Q9nar3 caenorhabdi
29	127	9.7	328	2	Q61XPO_CAEEL	Q61xpo caenorhabdi
30	127	9.7	1151	2	Q4RM11_TETNG	Q4rm11 tetraodon n
31	126.5	9.7	540	2	Q86Y22_HUMAN	Q86y22 homo sapien

ALIGNMENTS

RESULT 1		PRT; 243 AA.	
CTHR1_HUMAN	STANDARD;		
ID	Q96CG8; Q6TM91; Q8IX63;		
AC			
DT	10-MAY-2005 (Rel. 47, Created)		
DT	10-MAY-2005 (Rel. 47, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Collagen triple helix repeat-containing protein 1 precursor (NMTC1)		
DE	Protein.		
DE	Name=CTHR1; ORFNames=UNQ762/PRO1550;		
GN	Homo sapiens (Human).		
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.		
RC	TISSUE=Aorta;		
RX	PubMed=15618538; DOI=10.1161/01.RES.0000154262.07264.12;		
RA	Pyagay P., Herroult M., Wang Q., Lehner W., Belden J., Liaw L., Friessel R.E., Lindner V.,		
RA	"Novel polypeptide found in human cornea cDNA library."		
RA	"Collagen triple helix repeat containing 1, a novel secreted protein in injured and diseased arteries, inhibits collagen expression and promotes cell migration."		
RA	Circ. Res. 96:261-268(2005).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).		
RA	Sanuki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;		
RA	"Novel polypeptide found in human cornea cDNA library."		
RA	Submitted (JUN-2001) to the ENMB/GenBank/DDJB databases.		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).		
RX	PubMed=22975296; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Foster J.S., Grimaldi C., Gu J., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Shishajiri S., Sing J., Smith V., Stine J., Veltz A., Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.H., Yasuda D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.,		
RA	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment,"		
RT	Genome Res. 13:2226-2270(2003). /		
RL	RT		
RC	TISSUE=Kidney;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.L., Grouse F.S., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altenschul S.P., Zeeberg B., Buetow K.H., Schaefter C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		

RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakely R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smialius D.B., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [5]	QY	1 MRPOGPAASPORLRLGILLLQLPAPSSASEIPKGOKAQQLRQBVDLYNGMCLQGPAA 60		
RA	RP	PROTEIN SEQUENCE OF P31-45 (ISOFORM 1)	Db	1 MRPOGPAASPORLRLGILLLQLPAPSSASEIPKGOKAQQLRQBVDLYNGMCLQGPAA 60	
RX	PubMed=15340161; DOI=10.1101/ps.04682504;	QY	61 GVPGDGDSPGSANGTGTGIPGRDGFKGEGCECLRESFEESWTPYKQCSWSSLNQYIDL 120		
RX	RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites.", Protein Sci. 13:2819-2824(2004).	Db	61 GVPGDGDSPGSANGTGTGIPGRDGFKGEGCECLRESFEESWTPYKQCSWSSLNQYIDL 120	
CC	CC	-I- FUNCTION: May act as a negative regulator of collagen matrix deposition (By similarity).	AC	61 GVPGDGDSPGSANGTGTGIPGRDGFKGEGCECLRESFEESWTPYKQCSWSSLNQYIDL 120	
CC	CC	-I- SUBCELLULAR LOCATION: Secreted; extracellular (By similarity).	DT	10-MAY-2005 (Rel. 47, Created)	
CC	CC	-I- ALTERNATIVE PRODUCTS:	DT	10-MAY-2005 (Rel. 47, Last sequence update)	
CC	CC	Event-Alternative splicing: Named isoforms=2; Name=1;	DT	10-MAY-2005 (Rel. 47, Last annotation update)	
CC	CC	IsoId=Q96CG8-1; Sequence=Displayed;	DE	Collagen triple helix repeat-containing protein 1 precursor.	
CC	CC	Name=2;	GN	Name=Cthrc1;	
CC	CC	IsoId=Q96CG8-2; Sequence=vsp_013623; Sequence=vsp_013623;	OS	Rattus norvegicus (Rat)	
CC	CC	NOTE-NO experimental confirmation available; expressed in calcified tissue.	OC	Bukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Muridae; Murinae; Rattus.	
CC	CC	-I- TISSUE SPECIFICITY: Isoform 1 is expressed in calcified atherosclerotic plaque and chondrocyte-like cells.	OX	NCBI_TaxID=10116;	
CC	CC	-I- PTM: N-glycosylated (By similarity).	RN	[1]	
CC	CC	-I- SIMILARITY: Contains 1 collagen-like domain.	RP	NUCLEOTIDE SEQUENCE [mRNA], POSSIBLE FUNCTION, N-GLYCOSYLATION, RP INDUCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.	
CC	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	RC	STRAIN=Sprague-Dawley; TISSUE=Carotid artery;	
CC	CC	CC	Pubmed=15618538; DOI=10.1161/01.RSP.0000154262.07264.12;		
CC	CC	CC	Pyagay P., Herault M., Wang Q., Lehnert W., Beldien J., Liaw L., Friesele R.B., Lindner V.,		
CC	CC	CC	"Collagen triple helix repeat-containing 1, a novel secreted protein in injured and diseased arteries, inhibits collagen expression and promotes cell migration.", Circ. Res. 96:261-268 (2005).		
CC	CC	CC	-I- FUNCTION: Its overexpression in smooth muscle cell lines increases their migratory ability and inhibits collagen type I expression.		
CC	CC	CC	CC	May act as a negative regulator of extracellular matrix deposition.	
CC	CC	CC	CC	-I- SUBCELLULAR LOCATION: Secreted; extracellular	
CC	CC	CC	CC	-I- TISSUE SPECIFICITY: Expressed after injury in the carotid arteries (at protein level).	
CC	CC	CC	CC	CC	fibroblasts of the adventitia and the neointima of the arteries.
CC	CC	CC	CC	CC	-I- INDUCTION: Strongly induced in carotid arteries after injury (balloon catheter injury model). By various growth factor (BMP-4, TGF-beta1), in NIH3T3 cell line.
CC	CC	CC	CC	CC	-I- PTM: N-glycosylated.
CC	CC	CC	CC	CC	-I- SIMILARITY: Contains 1 collagen-like domain.
CC	CC	CC	CC	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	CC	CC	CC	CC	EMBL; AY136824; ANN15748.1; -; mRNA.
DR	DR	EMBL; AF395488; AA017919.1; -; mRNA.	DR	Ensembl; ENSRN00000004578; Rattus norvegicus.	
DR	DR	EMBL; AY358914; AAQ08273.1; -; mRNA.	DR	InterPro; IPR008161; C1g helix.	
DR	DR	EMBL; BC014245; AAH1425.1; -; mRNA.	DR	InterPro; IPR008160; Collagen.	
DR	DR	Ensembl; ENSG00000164932; Homo sapiens.	DR	Pfam; PF01391; Collagen 1.	
KW	KW	HGNC; HGNC:18831; CTHRC1.	DR	ProdDom; PDB00007; C1g_helix; 1.	
DR	DR	InteroPro; IPR008161; Collagen.	DR	Alternative splicing: Collagen; Direct protein sequencing;	
DR	DR	InteroPro; IPR008160; Collagen.	DR	Extracellular matrix; Glycoprotein; Signal; Structural protein.	
PT	PT	PT DOMAIN	PT	Collagen triple helix repeat-containing protein 1.	
PT	PT	PT CARBOHYD	PT	N-linked (GlcNAc, .) (Potential).	
PT	PT	PT VARSPLIC	PT	MRPOGPAASPORLRLGILLLQLPAPSSASEIPKGOKAQ	
PT	PT	PT SEQNEC	PT	LAPOREVND /FT1deVSP_013622.	
PT	PT	PT CONFICT	PT	K -> IYM_-(in isoform 2).	
PT	PT	PT SEQUENCE	PT	/FT1deVSP_013623.	
SQ	SQ	Score 100.0%; Pred. No. 2.e-107; Indels 0; Gaps 0;	DR	EMBL; AY136824; ANN15748.1; -; mRNA.	
Best Local Similarity 100.0%; Pred. No. 2.e-107; Indels 0; Gaps 0;	DR	Ensembl; ENSRN00000004578; Rattus norvegicus.			
Matches 243; Conservative 0; Mismatches 0;	DR	InterPro; IPR008161; C1g helix.			
Matches 243; Conservative 0; Mismatches 0;	DR	InterPro; IPR008160; Collagen.			
Matches 243; Conservative 0; Mismatches 0;	DR	Pfam; PF01391; Collagen 1.			
Matches 243; Conservative 0; Mismatches 0;	DR	ProdDom; PDB00007; C1g_helix; 1.			

KW	Collagen; Extracellular matrix; Glycoprotein; Signal;
STRUCTURAL PROTEIN.	Potential.
SIGNAL	1 32
FT CHAIN	33 245
FT DOMAIN	59 92
FT COORHID	188 188 (GICNAC. . .) (Potential).
SQ SEQUENCE	245 AA; 26424 MW; 2296F6DCDBA21F2 CRC64;
Query Match	94.0% Score 1225; DB 1; Length 245;
Best Local Similarity	94.7%; Pred. No. 1..8e-100;
Matches	3; Mismatches 8; Indels 2; Gaps 1;
Db	1 MRPGPASPQRURG--LILLILQLQPLAPSSASEIPIKGOKAQRLRQEVDLYNGMCLQ 58
Db	1 MRHQGRASPQLLQLQPLAPSSASEIPIKGOKAQRLRQEVDLYNGMCLQ 60
Qy	59 PACVPGRGSPGANGIPGTGPIGRDGKFGKECLRSFEESWTNYKOCSSWSSLNYGI 118
Db	61 PACVPGRGSPGANGIPGTGPIGRDGKFGKECLRSFEESWTNYKOCSSWSSLNYGI 120
Qy	119 DLGKIAETTPTKRSNSALRVLFGSLRLKCRNAACCWYFTNGAECGPPIEATYL 178
Db	121 DLGKIAETTPTKRSNSALRVLFGSLRLKCRNAACCWYFTNGAECGPPIEATYL 180
Qy	179 DOGSPEINSTINHTRSSVEGLCEGTGGAGLVDVAVWGTCSDPYPKGDASTGMNSVSRIII 238
Db	181 DOGSPEINSTINHTRSSVEGLCEGTGGAGLVDVAVWGTCSDPYPKGDASTGMNSVSRIII 240
Qy	239 BELPK 243
Db	241 BELPK 245
RESULT 3	
CTHRL MOUSE	STANDARD; PRT; 245 AA.
ID CTHRL MOUSE	STANDARD; PRT; 245 AA.
AC Q9D1D6;	47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)	
DT 10-MAY-2005 (Rel. 47, Last annotation update)	
DE Collagen triple helix repeat-containing protein 1 precursor.	
GN Cthrc1;	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC Muroidea; Muridae; Murinae; Mus.	
NCBI_TAXID=10090;	
RN [1]	RP NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;	
RX MEDLINE ID=2254683; Published=2005-05-01; DOI=10.1038/nature01266;	
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,	Qy
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,	Db
RA Yagi T., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,	Db
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	
RA Schriml L.M., Kanapin A., Matsuda H., Batyalov S., Beisel K.W.,	
RA Bratt D., Brusic V., Chothia C., Corbett L.E., Cousins S.,	
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	
RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.B.,	
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,	
RA Konagaya A., Kurchikian I.V., Lee Y., Lenhard B., Lyons P.A.,	
RA Magiold D.R., Marchionni L., McKenzie L., Mikl H.,	
RA Nagashima T., Numata K., Okido T., Pavan W.J., Peretea G.,	
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	
RA Ravasi T., Reed J.C., Reed D.J., Reid J.C., Ring B.Z., Ringwald M.,	
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,	
RA Sultan A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watcana Y.,	
RA Wilming L.G., Wyntshaw-Boris A., Yangnisawa M., Yang J., Yang L.,	
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	
RESULT 4	
Q5HZD2 XENTR PRELIMINARY; PRT; 258 AA.	
ID Q5HZD2;_XENTR PRELIMINARY; PRT; 258 AA.	
AC Q5HZD2;	
DT 10-MAY-2005 (TrEMBLrel. 30, Created)	
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)	
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)	
DE LOC54356 protein (Fragment).	
GN Xenopus tropicalis (Western clawed frog) (Siurana tropicalis).	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;	

OC	Xenopodinae; Xenopus; Silurana.		
NCBI_TaxID=8364;			
OX	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=whole body;		
RA	Straubenberg R.L., Feingold E.A., Collins F.S., Wagner L.H., Grouse L.H., Derge J.G., Klausner R.D., Schaefer C.F., Bhat N.K., Altschuler S.F., Zeiberg B., Buetow K.H., Moore T., Max S.I., Wang J.J., Hsieh F., Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Soares M.B., Stapleton M., Brownstein M.J., Uscio T.B., Toshiyuki S., Cabavat T.E., Brownstein N.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaracine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Paez J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.B., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Klein S., Gerard D.S.; Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: BC089073; AAH89073.1; -; mRNA.		
DR	GO: GO:0005737; :cytoplasm; IEA.		
DR	GO: GO:0006817; :phosphate transport; IEA.		
DR	InterPro: IPR008161; Clg_helix.		
DR	InterPro: IPR008160; Collagen.		
DR	Pfam: PF01391; Collagen_1.		
DR	ProDom: PD000007; Clg_helix_1.		
KW	Collagen.		
FT	NON_TER 1		
FT	NON_TER 191 191 191 AA; 20525 MW; CAB7BF4F582A3AA6 CRC64;		
SQ	SEQUENCE 258 AA; 28195 MW; F2E133341BA2CCA CRC64;		
Query Match	Score 992; DB 2; Length 258; Best Local Similarity 76.1%; Pred. No. 9.4e-80; Matches 183; Conservative 22; Mismatches 21; Indels 4; Gaps 3;		
Qy	16 LLLLIQLPAPSSASEIPKGKQKAQLRQRE--VYDVLGNGCLOPAGVPGRDGSFGANG 73		
Db	31 LVLCASLLPL-HSQPNQVQKRS-LRQKLDIERYNGICVQGAMGPPORDGTPGVNG 88		
Qy	74 IPGTPGPGRDGFKGFKCLESFESTWTNYKQCSWSSINYFTFNGAECCTKMR 133		
Db	89 IPGTPGPGRDGFKGFKCLESFESTWTNFQCAWSALINYGIDLGKLAECTTKMR 148		
Qy	134 NSALRVLFSGSLRLKCRNACCRWTFFNGECGSLPIEILYDQGSPMNSTINIR 193		
Db	149 HSALAVYUFGSGLRLKTRACCWRGTCSDYPKGDASTGWNNSVRIIEELPK 208		
Qy	194 TSSVEGLCEGIGAGLYDAIVWVGTCSDYPKGDASTGWNNSVRIIEELPK 243		
Db	209 TSTVEGLCEGIGAGLVDAVWVGTCSDYPKGDASTGWNNSVRIIEELPK 258		
RESULT 6	Q6AXL0_BPARE PRELIMINARY; ID OGAXL0_BPARE PRELIMINARY; AC OGAXL0; DT 25-OCT-2004 (TREMBLrel. 28, Created)		
Q4SM06	TETNG PRELIMINARY; ID Q4SM06_TETNG PRELIMINARY; AC Q4SM06; DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
AC	DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
DE	Chromosome 8 SCAP14545, whole genome shotgun sequence.		
DE	(Fragment)		
GN	ORFName=GSTENG00015647001;		
RESULT 5	Q6AXL0_BPARE PRELIMINARY; ID OGAXL0_BPARE PRELIMINARY; AC OGAXL0; DT 25-OCT-2004 (TREMBLrel. 28, Created)		
Q4SM06	TETNG PRELIMINARY; ID Q4SM06_TETNG PRELIMINARY; AC Q4SM06; DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
AC	DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DT	13-SEP-2005 (TREMBLrel. 31, Created)		
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)		
OS	Brachydanio rerio (Zebrafish) (Danio rerio)		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.		


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DR GO; GO:0006817; P:phosphate transport; TEA.
DR InterPro; IPR008161; C19 helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003161; FN_III_1.
DR InterPro; IPR003129; Laminin_G_TSP_N
DR InterPro; IPR002035; VWP_A.
DR Pfam; PF01391; Collagen; 4.
DR Pfam; PF00041; Err3; 6.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; WFADOMAIN.
DR ProDom; PD000007; C19 helix; 4.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50853; FN3; 6.
DR PROSITE; PS50234; VWFA; 1.
DR KW Collagen; Signal.
FT SIGNAL 1 28 Potential.
SEQUENCE 1472 AA; 156904 MW; 536611579C56FPD CRC64;

Query Match 10.1%; Score 131.5; DB 2; Length 1472;
Best Local Similarity 34.5%; Pred. No. 0.018; Gaps 6;
Matches 38; Conservative 7; Mismatches 26; Indels 39;
Qy 3 PQCPAAASSQRRLRQLLQLP-----APSSASET----PKGKQKAQLQREV 47
Db 11.61 PRPPPGSGGR-RG-----PGEQQEPGPKGEPGPCKVGPAGPSQQCSPGSQ--- 1207

Qy 48 VDLYNGMCLQGPAGVP-----GRDGSPGANGIPGTTGPIPGRDGFKEKG 91
Db 1208 -----GITIQGPVGPQGGKGERKDGTGSSGMQGIPGVQGAPGRDGLQGAKG 1252

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Search completed: April 20, 2006, 09:49:21
 Job time : 155.169 secs

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GenCore version 5.1.7
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1 protein - protein search, using sw model

Run on: April 20, 2006, 09:49:46 ; Search time 27.6353 Seconds
 (without alignments)
 726.976 Million cell updates/sec

Title: US-10-634-108-4
 Perfect score: 1303
 Sequence: 1 MRPQGPAAASPQRIGLILLL.....GDASTGWNNSVSRITIELPK 243

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6_ptodata/1/iaa/5_COMB.pep:
 2: /cgn2_6_ptodata/1/iaa/6_COMB.pep:
 3: /cgn2_6_ptodata/1/iaa/H_COMB.pep:
 4: /cgn2_6_ptodata/1/iaa/PCTUS_COMB.pep:
 5: /cgn2_6_ptodata/1/iaa/RE_COMB.pep:
 6: /cgn2_6_ptodata/1/iaa/backless..pep:
 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	243	2 US-09-692-081-4	Sequence 4, Appli
2	1300	99.8	243	2 US-09-692-081-4	Sequence 205, Appli
3	1294	99.3	243	2 US-09-692-081-4	Sequence 514, Appli
4	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
5	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
6	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
7	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
8	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
9	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
10	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
11	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
12	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
13	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
14	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
15	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
16	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
17	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
18	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
19	1294	99.3	243	2 US-09-692-081-4	Sequence 431, Appli
20	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
21	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
22	1294	99.3	243	2 US-09-692-081-4	Sequence 352, Appli
23	1225	94.0	245	2 US-09-692-081-4	Sequence 5, Appli
24	1225	94.0	277	2 US-09-692-081-4	Sequence 5, Appli
25	1109.5	85.1	276	2 US-09-692-081-4	Sequence 958, Appli
26	1109.5	85.1	276	2 US-09-692-081-4	Sequence 516, Appli
27	1046	80.3	197	2 US-09-692-081-4	Sequence 516, Appli

ALIGNMENTS

RESULT 1		RESULT 2	
US-09-692-081-4		US-09-489-847-205	
; Sequence 4, Application US/09692081		; Sequence 205, Application US/09489847	
; Patent No. 6630325		; Patent No. 6476195	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: LINDNER, Volkhard		; APPLICANT: Rosen et al	
; ATTORNEY: FRIESEL, Robert F.			
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL			
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)			
; CURRENT APPLICATION NUMBER: US-09/692,081			
; CURRENT FILING DATE: 2000-10-19			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 243			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-692-081-4		US-09-489-847-205	
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Best Local Matches	Similarity 100.0%;	Pred. No. 5.3e-125;	
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Db	1 MRPQGPASPORLRGLLILLQLPAPSSASEIPKGOKAOIPOREVYDLYNGCLOGP	1 MRPQGPASPORLRGLLILLQLPAPSSASEIPKGOKAOIPOREVYDLYNGCLOGP	1 MRPQGPASPORLRGLLILLQLPAPSSASEIPKGOKAOIPOREVYDLYNGCLOGP
QY	61 GVPGRDGSPPGANPGTGPPIPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL	61 GVPGRDGSPPGANPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL	61 GVPGRDGSPPGANPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL
Db	61 GVPGRDGSPPGANPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL	61 GVPGRDGSPPGANPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL	61 GVPGRDGSPPGANPGTGPPIGRDGFKGBCLEIRSEPESWTPNPKCQCSWSSINYGIDL
QY	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ
Db	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ	121 GKIAECTTGTNSNAIRVLFGSGSLRKCRNAACCQARYFTFNGAECGSPPLPIRRIYLDQ
QY	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE
Db	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE	181 GSPEMNSTINIHRTSSVEGLCEGLGAGLYDVAIWVGTCSDYPKGDASTGWNSVSRITIEE

; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031.P1
; CURRENT APPLICATION NUMBER: US/09/489, 847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094, 657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095, 486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096, 319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095, 454
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 205
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US -09-489-847-205

Query Match 99.8%; Score 1300; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 1..1e-124; Indels 0; Gaps 0;
Matches 242; Conservative 1; Missmatches 0;

Qy 1 MRPOGPAASPORLGRLLLLLQLPAPSSAEIPKGKQKAQLROREVVDLYNGMCLQGP 60
Db 1 MRPOGPAASPORLGRLLLLLQLPAPSSAEIPKGKQKAQLROREVVDLYNGMCLQGP 60

Qy 61 GVPGRDGSPANGIPTGPGRDKPKGECLRESFESWTNYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPANGIPTGPGRDKPKGECLRESFESWTNYKQCSWSSLNYGIDL 120

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Db 121 GKIACETFTKMRNSALRVLFGSGLRKERNACQWYTFENGACSGPLPIEAIYLQ 180

Qy 181 GSPEMNSTINHRHTSVEGLCEGAGLVDAIWGTCSDYPKGDASTGWNNSVRRIIE 240
Db 181 GSPEMNSTINHRHTSVEGLCEGAGLVDAIWGTCSDYPKGDASTGWNNSVRRIIE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 4
US-10-012-231A-352
; Sequence 352, Application US/10012231A
; Patent No. 692435
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bortstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paozi, Nicholas F.
; TITLE OF INVENTION: Secred and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
; FILE REFERENCE: P2810P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-012-231A-352

Query Match 99.3%; Score 1294; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 4..4e-124; Indels 0; Gaps 0;
Matches 242; Conservative 0; Missmatches 1;

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Db 1 MRPOGPAASPORLGRLLLLLQLPAPSSAEIPKGKQKAQLROREVVDLYNGMCLQGP 60

Qy 61 GVPGRDGSPANGIPTGPGRDKPKGECLRESFESWTNYKQCSWSSLNYGIDL 120
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Qy 121 GKIACETFTKMRNSALRVLFGSGLRKERNACQWYTFENGACSGPLPIEAIYLQ 180
Db 121 GKIACETFTKMRNSALRVLFGSGLRKERNACQWYTFENGACSGPLPIEAIYLQ 180

Qy 121 GKIACETFTKMRNSALRVLFGSGLRKERNACQWYTFENGACSGPLPIEAIYLQ 180
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RESULT 5
 US-10-012-231A-431
 ; Sequence 431, Application US/10012231A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillian, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; ACIDS Encoding the Same
 ; FILE REFERENCE: P2830PIC48
 ; CURRENT APPLICATION NUMBER: US/10/015,389A
 ; CURRENT FILING DATE: 2002-06-25
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO: 352
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-015-389A-352

Query Match 99.3%; Score 1294; DB 2; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.4e-124; Indels 0; Gaps 0;
 Matches 242; Conservative 0; Mismatches 0;

Qy 1 MRPGQPAASPORLRLGGLLQLPAPSSAEIPKGKQKAQLRQEVDVLYNGMCLQGP 60
 Db 1 MRPGQPAASPORLRLGGLLQLPAPSSAEIPKGKQKAQLRQEVDVLYNGMCLQGP 60

Qy 61 GVPGRDGSPPGANVPGTPGIPGRDGPKGEKGECLESFEESWTNPYKQCSNSSLNYGIDL 120
 Db 61 GVPGRDGSPPGANVPGTPGIPGRDGPKGEKGECLESFEESWTNPYKQCSNSSLNYGIDL 120
 Qy 61 GKIACETFTKRSNSAALRVFPGSLRLKCRNAACQWYFTNGAECSGPLPIEAIIYLDQ 180
 Db 121 GKIACETFTKRSNSAALRVFPGSLRLKCRNAACQWYFTNGAECSGPLPIEAIIYLDQ 180

Qy 121 GKIACETFTKRSNSAALRVFPGSLRLKCRNAACQWYFTNGAECSGPLPIEAIIYLDQ 180
 Db 121 GKIACETFTKRSNSAALRVFPGSLRLKCRNAACQWYFTNGAECSGPLPIEAIIYLDQ 180

Qy 121 GSPEMNSTINHRTSSVYGLCERGIGAGIVDVAIWVGTCSDYPKGDASTGWNNSVRRIEE 240
 Db 181 GSPEMNSTINHRTSSVYGLCERGIGAGIVDVAIWVGTCSDYPKGDASTGWNNSVRRIEE 240
 Qy 181 GSPEMNSTINHRTSSVYGLCERGIGAGIVDVAIWVGTCSDYPKGDASTGWNNSVRRIEE 240
 Db 181 GSPEMNSTINHRTSSVYGLCERGIGAGIVDVAIWVGTCSDYPKGDASTGWNNSVRRIEE 240

Qy 241 LPK 243
 Db 241 LPK 243

RESULT 6
 US-10-015-389A-352
 ; Sequence 352, Application US/10015389A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillian, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; ACIDS Encoding the Same
 ; FILE REFERENCE: P2830PIC48

CURRENT APPLICATION NUMBER: US/10/015,389A
 CURRENT FILING DATE: 2002-06-15
 PRIORITY APPLICATION removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO: 431
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-015-389A-431

Query Match 99.3%; Score 1294; DB 2; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.e-124;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60
 Db 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60

Qy 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180
 Db 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180

Qy 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180
 Db 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180

Qy 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240
 Db 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240

Qy 241 LPK 243
 Db 241 LPK 243

RESULT 9
 US-10-006-768A-431
 Sequence 431, Application US/10006768A
 Patent No. 6936637
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 Acids Encoding the Same

FILE REFERENCE: P2830P1C10
 CURRENT APPLICATION NUMBER: US/10/006,768A
 CURRENT FILING DATE: 2002-03-05
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 352
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-006-768A-431

Query Match 99.3%; Score 1294; DB 2; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.e-124;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60
 Db 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60

Qy 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180
 Db 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180

Qy 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240
 Db 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240

Qy 241 LPK 243
 Db 241 LPK 243

CURRENT APPLICATION NUMBER: US/10/015,389A
 CURRENT FILING DATE: 2002-06-15
 PRIORITY APPLICATION removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO: 431
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-006-768A-352

Query Match 99.3%; Score 1294; DB 2; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.e-124;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60
 Db 1 MRPOGPAASPORLRLQLLQLQDAPSSABIPKGKQQLRQEVDLYNGMCLQGA 60

Qy 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180
 Db 121 GKIACFTKMRNSNALSRLFKERNACQRWYFTENGAECSGPLPIEAIYLDQ 180

Qy 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240
 Db 181 GSPENNSTINHRTSVEGIGAGLIVDVAIWGTCSDPKGDASTGWNVSRIIIE 240

Qy 241 LPK 243
 Db 241 LPK 243

Db 241 LPK 243

RESULT 10
US-10-015-671A-352
Sequence 352, Application US/10015671A

GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2830PIC47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 431
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-015-671A-431

Query Match 99.3%; Score 1294; DB 2;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPQQPASPORLRGLLQLQLPAPSASETPKGKQAKLQRREVVDLYNGMCLQGP 60
Db 1 MRPQQPASPORLRGLLQLQLPAPSASETPKGKQAKLQRREVVDLYNGMCLQGP 60

Qy 61 GVPGRDGSPPGANGIPGTPGIPGDPFGEKGCLRSFEESTPNYKQCSNSSLNGLQDL 120
Db 61 GVPGRDGSPPGANGIPGTPGIPGDPFGEKGCLRSFEESTPNYKQCSNSSLNGLQDL 120

Qy 121 GKIACETFTKRSNSALRVLFGSGLRKCRNAACQWYFTPNAECGPLPIEAIIYLDQ 180
Db 121 GKIACETFTKRSNSALRVLFGSGLRKCRNAACQWYFTPNAECGPLPIEAIIYLDQ 180

Qy 181 GSPEMNSTINIRRTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGWNNSVRIIE 240
Db 181 GSPEMNSTINIRRTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGWNNSVRIIE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 12
US-10-015-393A-352
Sequence 352, Application US/10015393A

Patent No. 6351737
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2830PIC46
CURRENT APPLICATION NUMBER: US/10/015,393A
CURRENT FILING DATE: 2002-06-10
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 352
LENGTH: 243
TYPE: PRT

RESLT 11
US-10-015-671A-431
Sequence 431, Application US/10015671A

GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey

ORGANISM: Homo sapiens
US-10-015-393A-352

Query Match 99.3%; Score 1294; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60
Db 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60

Qy 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180
Db 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180

Qy 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180
Db 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180

Qy 181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVSRIIEE 240
Db 181 GSPEMNSTINHRTSSVEGLCEGIGAGLVDAIWGTCSDYPKGDASTGNNSVSRIIEE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 14
US-10-011-833A-352
; Sequence 352 ; Application US/10011833A
; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan J.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
; FILE REFERENCE: P28301C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-833A-352

Query Match 99.3%; Score 1294; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60
Db 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGPSPGANGIPTPGIFGRDGFKGEKGCLESFEESWTPNYKQCSWSSLNYIDL 120
Db 61 GVPGRDGPSPGANVIPTPGIFGRDGFKGEKGCLESFEESWTPNYKQCSWSSLNYIDL 120

Qy 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180
Db 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180

RESULT 15
US-10-011-833A-431
; Sequence 431 ; Application US/10011833A
; Patent No. 6951920

Query Match 99.3%; Score 1294; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60
Db 1 MRPGDGPASPORLRLGLLQLPAPSASEIPKGKQKAQLRQEVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGPSPGANGIPTPGIFGRDGFKGEKGCLESFEESWTPNYKQCSWSSLNYIDL 120
Db 61 GVPGRDGPSPGANVIPTPGIFGRDGFKGEKGCLESFEESWTPNYKQCSWSSLNYIDL 120

Qy 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180
Db 121 GKIACETFTKRSNSALRVLFGSGLRKCRNACCCRWYFTENGACSGPLPIEATIYLQDQ 180

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Perrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Peoni, Nicholas P.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C22
 CURRENT APPLICATION NUMBER: US/10/011,833A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 431
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-011-833A-431

Query Match 99.3% Score 1294; DB 2; Length 243;

Best Local Similarity 99.6% Pred. No. 4.e-124;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MHQGPAASPORTGLLILLLQLPAPSSASEIPKGKOKAQLRQREVDLYNGMCLQGPA	60
Db	1	MHQGPAASPORTGLLILLLQLPAPSSASEIPKGKOKAQLRQREVDLYNGMCLQGPA	60
Qy	61	GVPGRDGPGANGIPGTGIPGRDGPKGSEKGECLRESFEESWTPNKCSWSSLNTYIDL	120
Db	61	GVPGRDGPGANGIPGTGIPGRDGPKGSEKGECLRESFEESWTPNKCSWSSLNTYIDL	120
Qy	121	GKIAECTPKRSNSALRVLFSGSLRLKCRNACQCRWYFTFNGAECSGPLPIEAIIYLQDQ	180
Db	121	GKIAECTPKRSNSALRVLFSSSLRLKCRNACQCRWYFTFNGAECSGPLPIEAIIYLQDQ	180
Qy	181	GSPBMNSTINIRHTSSVPLCIGIGAGLYDAIWVGTCSDYPKGDASTGNNSVSRIIEE	240
Db	181	GSPBMNSTINIRHTSSVPLCIGIGAGLYDAIWVGTCSDYPKGDASTGNNSVSRIIEE	240
Qy	241	LPK 243	
Db	241	LPK 243	

Search completed. April 20, 2006, 09:52:00
 Job time : 28.633 secs

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OM protein - protein search, using sw model

Run on: April 20, 2006, 09:52:21 ; Search time 13.9765 Seconds

(without alignments)
765.051 Million cell updates/sec

Title: US-10-634-108-4

Perfect score: 1.303

Sequence: 1 MRPQSPAAASPQRRLRGLLIL.....GDASTGWNNSVSRRIEELPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters:

225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA_New.*

1: /SIDSS/pctodata/2/pubpa/us08_new_pub.pep:*

2: /SIDSS/pctodata/2/pubpa/us06_new_pub.pep:*

3: /SIDSS/pctodata/2/pubpa/us07_new_pub.pep:*

4: /SIDSS/pctodata/2/pubpa/pct_new_pub.pep:*

5: /SIDSS/pctodata/2/pubpa/us09_new_pub.pep:*

6: /SIDSS/pctodata/2/pubpa/us10_new_pub.pep:*

7: /SIDSS/pctodata/2/pubpa/us11_new_pub.pep:*

8: /SIDSS/pctodata/2/pubpa/us60_new_pub.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.03	100.0	278	7 US-11-186-284-77	Sequence 77, App1
2	13.00	99.8	243	7 US-11-223-769-205	Sequence 205, App1
3	12.98	99.6	243	7 US-11-080-991-14	Sequence 14, App1
4	12.94	99.3	243	6 US-10-053-703-122	Sequence 122, App1
5	12.94	99.3	243	6 US-10-194-487-366	Sequence 366, App1
6	12.94	99.3	243	6 US-10-195-983-366	Sequence 366, App1
7	12.94	99.3	243	6 US-10-195-888-366	Sequence 366, App1
8	12.94	99.3	243	6 US-10-195-889-366	Sequence 366, App1
9	12.94	99.3	243	7 US-11-102-240-122	Sequence 122, App1
10	12.94	99.3	243	7 US-11-103-195-122	Sequence 122, App1
11	12.94	99.3	243	7 US-11-226-869-514	Sequence 514, App1
12	12.94	99.3	278	7 US-11-226-869-515	Sequence 515, App1
13	10.46	80.3	197	7 US-11-226-869-516	Sequence 516, App1
14	10.46	80.3	232	7 US-11-226-869-517	Sequence 517, App1
15	24.8	19.0	46	7 US-11-226-869-518	Sequence 518, App1
16	15.6	15.0	93	7 US-11-229-769-240	Sequence 240, App1
17	19.6	15.0	93	7 US-11-223-769-362	Sequence 362, App1
18	14.1	10.8	26	7 US-11-226-869-519	Sequence 519, App1
19	12.95	9.9	585	6 US-10-508-440-2	Sequence 2, App1
20	12.9	9.9	287	7 US-11-174-150-30	Sequence 30, App1
21	127.5	9.8	1464	6 US-10-501-035-331	Sequence 331, App1
22	127.5	9.8	1464	7 US-11-000-463-243	Sequence 243, App1
23	127.5	9.8	1464	7 US-11-186-284-28	Sequence 28, App1
24	127.5	9.8	1464	7 US-11-021-603-2	Sequence 2, App1
25	127.5	9.8	1467	6 US-10-821-234-1096	Sequence 1096, App1

ALIGNMENTS

RESULT 1 US-11-186-284-77 ; Sequence 77, Application US/11186284 ; Publication No. US20050266493A1 ; GENERAL INFORMATION: ; APPLICANT: Millennium Pharmaceuticals, Inc. ; APPLICANT: Berger, Allison ; APPLICANT: Guillemette, Tracy L. ; APPLICANT: Kamatkar, Shubhangi ; APPLICANT: Schlesel, Robert ; APPLICANT: Monahan, John R. ; APPLICANT: Thibodeau, Stephen N. ; APPLICANT: Burhart, Lawrence J. ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF COLON CANCER ; TITLE OF INVENTION: THERAPY OF COLON CANCER ; FILE REFERENCE: MEM01-029PRNM ; CURRENT APPLICATION NUMBER: US/11/186-284 ; CURRENT FILING DATE: 2005-07-21 ; PRIORITY APPLICATION NUMBER: US/10/301,822 ; PRIORITY FILING DATE: 2002-11-11 ; PRIORITY APPLICATION NUMBER: US 60/339,971 ; PRIORITY FILING DATE: 2001-12-10 ; PRIORITY APPLICATION NUMBER: US 60/361,978 ; PRIORITY FILING DATE: 2002-03-05 ; PRIORITY APPLICATION NUMBER: US 60/381,988 ; PRIORITY FILING DATE: 2002-05-20 ; NUMBER OF SEQ ID NOS: 228 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 77 ; LENGTH: 278 ; TYPE: PRT ; ORGANISM: Homo Sapiens ; US-11-186-284-77
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Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 1303; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.7e-116;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-11-229-769-205
 Sequence 205, Application US/11229769
 Publication No. US20060079670A1
 GENERAL INFORMATION:
 APPLICANT: Komatsoulis et al
 TITLE OF INVENTION: 98 Human Secreted Proteins
 FILE REFERENCE: P2031PD1C1
 CURRENT APPLICATION NUMBER: US/11/229,769
 CURRENT FILING DATE: 2005-09-20
 PRIOR APPLICATION NUMBER: 10/233,453
 PRIOR FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 09/489,847
 PRIOR FILING DATE: 2000-01-24
 PRIOR APPLICATION NUMBER: PCT/US99/17130
 PRIOR FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 60/094,657
 PRIOR FILING DATE: 1998-07-31
 PRIOR APPLICATION NUMBER: 60/095,486
 PRIOR FILING DATE: 1998-08-05
 PRIOR APPLICATION NUMBER: 60/095,319
 PRIOR FILING DATE: 1998-08-12
 PRIOR APPLICATION NUMBER: 60/095,454
 PRIOR FILING DATE: 1998-08-06
 PRIOR APPLICATION NUMBER: 60/095,455
 PRIOR FILING DATE: 1998-08-06
 NUMBER OF SEQ ID NOS: 376
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 205
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo sapiens
 us-11-229-769-205

Query Match 99.8%; Score 1300; DB 7; Length 243;
 Best Local Similarity 99.6%; Pred. No. 4.4e-116;
 Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLQLGLLQLQLPAPSASBIPKGKQAKLQREVDLYNGMCLQGPAA 60
 Db 1 MRPOGPAASPORLQLGLLQLQLPAPSASBIPKGKQAKLQREVDLYNGMCLQGPAA 60
 Qy 1 GVPGRDGSPGANGIPTGPIGTRDFGKGEKGCRESFEESWTNPVKQCSWSSLNYGIDL 120
 Db 1 GVPGRDGSPGANGIPTGPIGTRDFGKGEKGCRESFEESWTNPVKQCSWSSLNYGIDL 120
 Qy 1 GVPGRDGSPGANGIPTGPIGTRDFGKGEKGCRESFEESWTNPVKQCSWSSLNYGIDL 120
 Db 1 GVPGRDGSPGANGIPTGPIGTRDFGKGEKGCRESFEESWTNPVKQCSWSSLNYGIDL 120
 Qy 1 GKIACETFTKRSNSALRVLFGSRLKCRNACCRWYFTENGACSGPLPIEATIYLDQ 180
 Db 1 GKIACETFTKRSNSALRVLFGSRLKCRNACCRWYFTENGACSGPLPIEATIYLDQ 180
 Qy 181 GSPENNSTINHRTSSVEGLCEGTAGLVDVIAWGTCSDPKGASTGIVNSVSIIIE 240
 Db 181 GSPENNSTINHRTSSVEGLCEGTAGLVDVIAWGTCSDPKGASTGIVNSVSIIIE 240
 Qy 241 LPK 243
 Db 241 LPK 243

RESULT 4
 US-10-063-703-122
 Sequence 122, Application US/10063703
 Publication No. US2006008901A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurine, Austin L.
 APPLICANT: Wattanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P323081C1
 CURRENT APPLICATION NUMBER: US/10/063,703
 CURRENT FILING DATE: 2002-05-08
 Prior Application removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO: 122
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo sapiens
 us-10-063-703-122

Query Match 99.3%; Score 1294; DB 6; Length 243;

RESULT 3
 US-11-080-991-14

Best Local Similarity 99.6%; Pred. No. 1.6e-115; Mismatches 0; Indels 1; Gaps 0;

Query 1 MRPGQPAASPORLQLLQLQPPASAEPKGKQKAQIRQREVVLDYNGMCLOQPA 60
Db 1 MRPGQPAASPORLQLLQLQPPASAEPKGKQKAQIRQREVVLDYNGMCLOQPA 60
Qy 61 GVPGRDGSPPGANG1PCTPGRDGPKFGEKGCLIRESPESWTPNYKOCWSSSLNTYIDL 120
Db 61 GVPGRDGSPPGANG1PCTPGRDGPKFGEKGCLIRESPESWTPNYKOCWSSSLNTYIDL 120
Qy 121 GKIAEACTKMRNSNLSALRVLFGSISRLKCRNAACQRWYFTENGAECSGPLPIEAIIYLDQ 180
Db 121 GKIAEACTKMRNSNLSALRVLFGSISRLKCRNAACQRWYFTENGAECSGPLPIEAIIYLDQ 180
Qy 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240
Db 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240
Qy 241 LPK 243
Db 241 LPK 243
Qy 241 LPK 243
Db 241 LPK 243

RESULT 5
US-10-194-487-366
; Sequence 366, Application US/101944487
; Publication No. US200600742267A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: P3430R1C323
; CURRENT FILING DATE: 2002-07-15
; PRIORITY NUMBER: 10/052586
; PRIORITY FILING DATE: 2002-01-15
; PRIORITY APPLICATION NUMBER: 60/059263
; PRIORITY APPLICATION NUMBER: 60/059266
; PRIORITY FILING DATE: 1997-09-18
; PRIORITY APPLICATION NUMBER: 60/062250
; PRIORITY FILING DATE: 1997-10-17
; PRIORITY APPLICATION NUMBER: 60/063120
; PRIORITY APPLICATION NUMBER: 60/063121
; PRIORITY FILING DATE: 1997-10-24
; PRIORITY APPLICATION NUMBER: 60/063486
; PRIORITY FILING DATE: 1997-10-21
; PRIORITY APPLICATION NUMBER: 60/063540
; PRIORITY APPLICATION NUMBER: 60/063541
; PRIORITY FILING DATE: 1997-10-28
; PRIORITY APPLICATION NUMBER: 60/063544
; PRIORITY FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-883-366

RESULT 6
US-10-195-883-366
; Sequence 366, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195-883
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-883-366

Query Match 99.3%; Score 1294; DB 6; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.6e-115; Mismatches 0; Indels 1; Gaps 0;

Query 1 MRPGQPAASPORLQLLQLQPPASAEPKGKQKAQIRQREVVLDYNGMCLOQPA 60
Db 1 MRPGQPAASPORLQLLQLQPPASAEPKGKQKAQIRQREVVLDYNGMCLOQPA 60
Qy 61 GVPGRDGSPPGANG1PCTPGRDGPKFGEKGCLIRESPESWTPNYKOCWSSSLNTYIDL 120
Db 61 GVPGRDGSPPGANG1PCTPGRDGPKFGEKGCLIRESPESWTPNYKOCWSSSLNTYIDL 120
Qy 121 GKIAEACTKMRNSNLSALRVLFGSISRLKCRNAACQRWYFTENGAECSGPLPIEAIIYLDQ 180
Db 121 GKIAEACTKMRNSNLSALRVLFGSISRLKCRNAACQRWYFTENGAECSGPLPIEAIIYLDQ 180
Qy 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240
Db 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240
Qy 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240
Db 181 GSPEMNSTINHRTSSVEGLCERIGAGLIVDVAIWVGTCSDYPKGDASTGWNSVSRIIE 240

QY 241 LPK 243
Db 241 LPK 243

RESULT 7
US-10-195-888-366
Sequence 366, Application US/10195888
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanaabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C324
CURRENT APPLICATION NUMBER: US/10/195,888
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO: 366
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-195-888-366

Query Match 99.3%; Score 1294; DB 6; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.6e-115;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPOGPAAASPORLQLLQLLPAPSABEPKQKQALQREVVLDLYNGMCLQGPA 60
Db 1 MRPOGPAAASPORLQLLQLLPAPSABEPKQKQALQREVVLDLYNGMCLQGPA 60

Qy 1 MRPOGPAAASPORLQLLQLLPAPSABEPKQKQALQREVVLDLYNGMCLQGPA 60
Db 1 MRPOGPAAASPORLQLLQLLPAPSABEPKQKQALQREVVLDLYNGMCLQGPA 60

Qy 61 GVPGRDGSPGANGIPGTGIPGRDFGPKGECKECLRSFEETWTPNYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPGANGIPGTGIPGRDFGPKGECKECLRSFEETWTPNYKQCSWSSLNYGIDL 120

Qy 61 GVPGRDGSPGANGIPGTGIPGRDFGPKGECKECLRSFEETWTPNYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPGANGIPGTGIPGRDFGPKGECKECLRSFEETWTPNYKQCSWSSLNYGIDL 120

Qy 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTENGAECSGPLPIEATIYLQ 180
Db 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTENGAECSGPLPIEATIYLQ 180

Qy 181 GSPEMNSTINHRTSSVEGLCEGIGLVDVIAIWGTCSDYPKGDASTGWNNSVRRIEE 240
Db 181 GSPEMNSTINHRTSSVEGLCEGIGLVDVIAIWGTCSDYPKGDASTGWNNSVRRIEE 240

Qy 241 LPK 243
Db 241 LPK 243

Qy 241 LPK 243
Db 241 LPK 243

RESULT 9
US-11-102-240-122
Sequence 122, Application US/11/022440
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/033662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/233328
SEQ ID NO: 122
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-122

Query Match 99.3%; Score 1294; DB 7; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.6e-115;

RESULT 8
US-10-195-888-366
Sequence 366, Application US/10195888
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria

Query Match 99.3%; Score 1294; DB 7; Length 278;
 Best Local Similarity 99.0%; Pred. No. 1.9e-11;
 Matches 242; Conservative 0; Indels 0; Gaps 0;
 SEQ ID NO: 516

Qy 1 MRPGPAAASPORLGLLQLQLPAPSABIPKQKQAKLQRREVVDLYNGMCLOGPA 60
 Db 36 MRPGPAAASPORLGLLQLQLPAPSABIPKQKQAKLQRREVVDLYNGMCLOGPA 95

Qy 61 GVPGRDGSPGANGIPGPIPERDGPKGEKBCELRESFEETWPNYKQCSWSSLNYGIDL 120
 Db 96 GVPGRDGSPGANVIPGTPGPIPERDGPKGEKBCELRESFEETWPNYKQCSWSSLNYGIDL 155

Qy 121 GKIAECTFTKMRNSALRVLFSGSLRKCRNACCORWFTEGAECGPLPIEATIYLDQ 180
 Db 156 GKIAECTFTKMRNSALRVLFSGSLRKCRNACCORWFTEGAECGPLPIEATIYLDQ 215

Qy 181 GSPENNSTINHRTSSVGLCEGGAGLVDVIAWGTCDYKGDASTGMNSVRRIEE 240
 Db 216 GSPENNSTINHRTSSVGLCEGGAGLVDVIAWGTCDYKGDASTGMNSVRRIEE 275

RESULT 13
 US-11-226-869-516
 ; Sequence 516, Application US/11226869
 ; Publication No. US20060069054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Perbing, David H.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.470C14
 ; CURRENT FILING DATE: 2005-09-13
 ; NUMBER OF SEQ ID NOS: 627
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 516
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-226-869-516

Query Match 80.3%; Score 1046; DB 7; Length 197;
 Best Local Similarity 99.5%; Pred. No. 4.7e-92;
 Matches 196; Conservative 0; Indels 0; Gaps 0;
 SEQ ID NO: 516

Qy 1 MRPGPAAASPORLGLLQLQLPAPSABIPKQKQAKLQRREVVDLYNGMCLOGPA 60
 Db 1 MRPGPAAASPORLGLLQLQLPAPSABIPKQKQAKLQRREVVDLYNGMCLOGPA 60

Qy 61 GVPGRDGSPGANGIPGPIPERDGPKGEKBCELRESFEETWPNYKQCSWSSLNYGIDL 120
 Db 61 GVPGRDGSPGANGIPGPIPERDGPKGEKBCELRESFEETWPNYKQCSWSSLNYGIDL 120

Qy 121 GKIAECTFTKMRNSALRVLFSGSLRKCRNACCORWFTEGAECGPLPIEATIYLDQ 180
 Db 121 GKIAECTFTKMRNSALRVLFSGSLRKCRNACCORWFTEGAECGPLPIEATIYLDQ 180

Qy 181 GSPENNSTINHRTSSV 197
 Db 181 GSPENNSTINHRTSSV 197

RESULT 14
 US-11-226-869-517
 ; Sequence 517, Application US/11226869
 ; Publication No. US20060069054A1
 ; GENERAL INFORMATION:

Search completed: April 20, 2006, 09:57:47
 Job time : 15.9765 secs

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OM protein - protein search, using sw model

Run on: April 20, 2006, 09:50:45 ; Search time 92.1176 Seconds
 (without alignments)
 1102.205 Million cell updates/sec

Title: US-10-634-108-4

Perfect score: 1303

Sequence: 1 MRPDSPAAASPRQRGLLML.....GDASTGWNNSVSRRIIELPK 243

Scoring table: BLOSUM62

Gapext: 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA_Main:*

1: /cgmn_2/_ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgmn_6/_ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgmn_6/_ptodata/1/pubpaa/US10_PUBCOMB.pep:*

4: /cgmn_6/_ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgmn_6/_ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgmn_6/_ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1303	100.0	243	3 US-10-822-472B-19	Sequence 19, Appli
2	1303	100.0	243	4 US-10-045-992-4	Sequence 4, Appli
3	1303	100.0	243	4 US-10-030-135	Sequence 135, Appli
4	1303	100.0	243	4 US-10-295-027-50	Sequence 50, Appli
5	1303	100.0	243	4 US-10-295-027-1173	Sequence 1173, Appli
6	1303	100.0	243	4 US-10-173-999-74	Sequence 74, Appli
7	1303	100.0	243	4 US-10-058-270A-38	Sequence 38, Appli
8	1303	100.0	243	4 US-10-634-108-4	Sequence 4, Appli
9	1303	100.0	243	4 US-10-188-32-175	Sequence 175, Appli
10	1303	100.0	243	5 US-10-939-233-4	Sequence 4, Appli
11	1303	100.0	243	6 US-11-050-926-135	Sequence 135, Appli
12	1303	100.0	278	4 US-10-097-30-131	Sequence 131, Appli
13	1303	100.0	278	4 US-10-177-293-496	Sequence 496, Appli
14	1303	100.0	278	4 US-10-301-822-77	Sequence 77, Appli
15	1303	100.0	278	4 US-10-296-115-1261	Sequence 1261, Appli
16	1303	100.0	278	5 US-10-961-139-2	Sequence 2, Appli
17	1303	100.0	278	6 US-11-050-926-131	Sequence 131, Appli
18	1300	99.8	278	4 US-10-097-30-131	Sequence 131, Appli
19	1300	99.8	278	4 US-10-060-036-4551	Sequence 4551, Appli
20	1298	99.6	243	4 US-10-176-847-14	Sequence 14, Appli
21	1294	99.3	243	3 US-19-83-759-514	Sequence 514, Appli
22	1294	99.3	243	3 US-09-938-418-7	Sequence 7, Appli
23	1294	99.3	243	3 US-09-946-374-352	Sequence 352, Appli
24	1294	99.3	243	3 US-09-946-374-431	Sequence 431, Appli
25	1294	99.3	243	4 US-10-006-867-122	Sequence 122, Appli
26	1294	99.3	243	4 US-10-032-586-366	Sequence 366, Appli
27	1294	99.3	243	4 US-10-007-805-514	Sequence 514, Appli

ALIGNMENTS

RESULT 1
 US-09-829-472A-19
 / Sequence 19, Application US/09829472A
 / Publication No. US20040146862A1
 / GENERAL INFORMATION:
 / APPLICANT: Mack, David
 / APPLICANT: Gish, Kurt
 / APPLICANT: BOS Biotechnology, Inc.
 / TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and Methods of Screening for Modulators of Breast Cancer
 / FILE REFERENCE: 018501.01200US
 / CURRENT APPLICATION NUMBER: US/09-822,472A
 / CURRENT FILING DATE: 2001-04-09
 / PRIOR APPLICATION NUMBER: US 09/525,361
 / PRIORITY FILING DATE: 2000-03-15
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 19
 / LENGTH: 243
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: BCN4, ESTB, secreted protein
 / OTHER INFORMATION: US-09-829-472A-19

(D/C)

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 20, 2006, 09:50:45 ; Search time 92.1176 Seconds
(without alignment)
1102.205 Million cell updates/sec

Title: US-10-634-108-4
Perfect score: 1303
Sequence: 1 MRQQPAAASFQRRLQLLIL.....GDASTGNNSVSRRIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	243	3	US-09-829-472A-19
2	1303	100.0	243	4	US-10-045-992-4
3	1303	100.0	243	4	US-10-057-340-135
4	1303	100.0	243	4	US-10-295-027-50
5	1303	100.0	243	4	US-10-295-027-1173
6	1303	100.0	243	4	US-10-177-999-24
7	1303	100.0	243	4	US-10-057-270A-38
8	1303	100.0	243	4	US-10-634-108-4
9	1303	100.0	243	4	US-10-188-332-175
10	1303	100.0	243	5	US-10-939-233-4
11	1303	100.0	243	6	US-11-059-926-135
12	1303	100.0	278	4	US-10-097-340-131
13	1303	100.0	278	4	US-10-177-293-496
14	1303	100.0	278	4	US-10-301-822-77
15	1303	100.0	278	4	US-10-196-115-1261
16	1303	100.0	278	5	US-10-967-139-2
17	1303	100.0	278	6	US-11-059-926-131
18	1300	99.8	278	4	US-10-351-334-205
19	1300	99.8	278	4	US-10-060-036-4551
20	1298	99.6	243	4	US-10-177-847-14
21	1294	99.3	243	3	US-09-834-759-514
22	1294	99.3	243	3	US-09-938-418-7
23	1294	99.3	243	3	US-09-948-374-352
24	1294	99.3	243	3	US-09-946-374-431
25	1294	99.3	243	4	US-10-006-867-122
26	1294	99.3	243	4	US-10-052-586-366
27	1294	99.3	243	4	US-10-007-805-514

ALIGNMENTS

RESULT 1
US-09-829-472A-19

; Sequence 19, Application US/09829472A
; Publication No. US0040146862A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: BOS Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-001200US
; CURRENT APPLICATION NUMBER: US/09/829,472A
; CURRENT FILING DATE: 2001-04-09
; PRIORITY APPLICATION NUMBER: US 09/525,361
; PRIORITY FILING DATE: 2000-03-15 (O2C)
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO.: 19
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BCM4, ESTB, secreted protein
US-09-829-472A-19

Query Match 100.0%; Score 1303; DB 3; Length 243;
Best Local Similarity 100.0%; pred. No. 1..6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRQGPAAASPORGLLILLIQLPAPSSAEIPKGOKAQRLREVVDLYNGMCLQGPAA 60
Db 1 MRQGPAAASPORGLLILLIQLPAPSSAEIPKGOKAQRLREVVDLYNGMCLQGPAA 60

Qy 61 GYPRGDGSPGPNAGCTPGTPGIPGRDGFKEKGCLTRESFEESWTPNYKOCWSLNYGIDL 120
Db 61 GYPRGDGSPGPNAGCTPGTPGIPGRDGFKEKGCLTRESFEESWTPNYKOCWSLNYGIDL 120

Qy 121 GKIAECTFTKMRNSNIALRVLFGSGLRKCRNACCRQNYFTENGAECGPLPLFALIYLDQ 180
Db 121 GKIAECTFTKMRNSNIALRVLFGSGLRKCRNACCRQNYFTENGAECGPLPLFALIYLDQ 180

RESULT 2
US-10-045-992-4
Sequence 4, Application US/10045992
Publication No. US2002016121A1
GENERAL INFORMATION:
APPLICANT: LINDNER, Volkhard
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODELIN
FILE REFERENCE: 053689-5006-01
CURRENT APPLICATION NUMBER: US/10/045,992
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 09/692,081
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-045-992-4

Query Match 100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 243; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MRPOGPAASPORLGRGLLQLPAPSASBIPKSKOKAQLRQEVDLYNGMCLQGP 60
Db 1 MRPOGPAASPORLGRGLLQLPAPSASBIPKSKOKAQLRQEVDLYNGMCLQGP 60

Qy 61 GVPGRDGSPGANGIPTGPGRDGPKGEKGECLESFEESSWTPNYKOCSSSLINYGIDL 120
Db 61 GVPGRDGSPGANGIPTGPGRDGPKGEKGECLESFEESSWTPNYKOCSSSLINYGIDL 120

Qy 121 GKIACETFTKMRNSALRVLFSGSLRKCRNACQRYWTFNGAECGPLPIEATIYLQ 180
Db 121 GKIACETFTKMRNSALRVLFSGSLRKCRNACQRYWTFNGAECGPLPIEATIYLQ 180

Qy 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGNSVSRILIEE 240
Db 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGNSVSRILIEE 240

Qy 241 LPK 243
Db 241 LPK 243

Query Match 100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 243; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MRPOGPAASPORLGRGLLQLPAPSASBIPKSKOKAQLRQEVDLYNGMCLQGP 60
Db 1 MRPOGPAASPORLGRGLLQLPAPSASBIPKSKOKAQLRQEVDLYNGMCLQGP 60

Qy 61 GVPGRDGSPGANGIPTGPGRDGPKGEKGECLESFEESSWTPNYKOCSSSLINYGIDL 120
Db 61 GVPGRDGSPGANGIPTGPGRDGPKGEKGECLESFEESSWTPNYKOCSSSLINYGIDL 120

Qy 121 GKIACETFTKMRNSALRVLFSGSLRKCRNACQRYWTFNGAECGPLPIEATIYLQ 180
Db 121 GKIACETFTKMRNSALRVLFSGSLRKCRNACQRYWTFNGAECGPLPIEATIYLQ 180

Qy 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGNSVSRILIEE 240
Db 181 GSPEMNSTINIRHTSSVEGLCEGIGAGLVDAIWGTCSDPKGDASTGNSVSRILIEE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 3
US-10-097-340-135
Sequence 135, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAM
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, JR.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025

RESULT 4
US-10-295-027-50
Sequence 50, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezsi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and METHODS OF SCREENING FOR MODULATORS OF CANCER
FILE REFERENCE: 018501-012500US
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464

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; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 50
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-50

US-10-295-027-50          Query Match          100.0% Score 1303; DB 4; Length 243;
Best Local Similarity      100.0% Pred. No 1, 6e-115; Mismatches 0; Indels 0; Gaps 0
Matches 243; Conservative 0; Gapopen 0; Gapclose 0

1 MRPOGPAASPORLGRILLQLPAPSSASEIPKGKQKAQLRQEYVVLQYNGMCLOGG
1 MRPOGPAASPORLGRILLQLPAPSSASEIPKGKQKAQLRQEYVVLQYNGMCLOGG
1 GVPGRDGSPGANGITPGTPGIPGRDFKGKGECLRESFEESTPNYKQCSWSSLNYGIL
1 GVPGRDGSPGANGITPGTPGIPGRDFKGKGECLRESFEESTPNYKQCSWSSLNYGIL
121 GKIACETFTKMRNSALRVLFSGSLRLKCRNACCCRWTFGNGAECGCGPLPIEATIYL
121 GKIACETFTKMRNSALRVLFSGSLRLKCRNACCCRWTFGNGAECGCGPLPIEATIYL
61 GSPENNSTINHRRTSSVEGLCEGAGLVDIAWGTCDYPKGCDASTGNSVSRRIIE
61 GSPENNSTINHRRTSSVEGLCEGAGLVDIAWGTCDYPKGCDASTGNSVSRRIIE
121 GKIACETFTKMRNSALRVLFSGSLRLKCRNACCCRWTFGNGAECGCGPLPIEATIYL
121 GKIACETFTKMRNSALRVLFSGSLRLKCRNACCCRWTFGNGAECGCGPLPIEATIYL
181 GSPENNSTINHRRTSSVEGLCEGAGLVDIAWGTCDYPKGCDASTGNSVSRRIIE
181 GSPENNSTINHRRTSSVEGLCEGAGLVDIAWGTCDYPKGCDASTGNSVSRRIIE
241 LPK 243
241 LPK 243
241 LPK 243

REBESULT 5
US-10-295-027-1173          Sequence 1173, Application US/10295027
; GENERAL INFORMATION:
; Publication No. US20100232350A1
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezsi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-0125001US
; CURRENT APPLICATION NUMBER: US/10-295, 027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15

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; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1173
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-1173

Query Match          100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRPOCPAASPORLGLLILLQLPAPSSSEIIPKGKQAKLQRBEVVDLYNGMCILQGPA 60
Db      1 MRPOCPAASPORLGLLILLQLPAPSSSEIIPKGKQAKLQRBEVVDLYNGMCILQGPA 60
Qy      61 GVPGRDGSPPANGIFPTPGIPGRDGFKEGECLRESFESWTPNYKQCSWSSLNYYGIDL 120
Db      61 GVPGRDGSPPANGIFPTPGIPGRDGFKEGECLRESFESWTPNYKQCSWSSLNYYGIDL 120
Qy      121 GKIACTETFKMRNSALRVLFGSLRLKERNACCRWYFFNGAFCSGPLIEATLYLDQ 180
Db      121 GKIACTETFKMRNSALRVLFGSLRLKERNACCRWYFFNGAFCSGPLIEATLYLDQ 180
Qy      181 GSPENMNSTINHRPSSVEGLCEGIGAGLDVAVIWTCSDPYPKGDASTGNNSVSRIIEE 240
Db      181 GSPENMNSTINHRPSSVEGLCEGIGAGLDVAVIWTCSDPYPKGDASTGNNSVSRIIEE 240
Qy      241 LPK 243
Db      241 LPK 243

RESULT 6
US-10-173-999-74
Sequence 74, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-00242015
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74

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LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-173-99-74

Query Match 100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1..6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLQLLQLQLPAPSASEIPKQKAOLQREVVDLYNGMCLQGPA 60
Db 1 MRPOGPAASPORLQLLQLQLPAPSASEIPKQKAOLQREVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGSPGANGIPCTPGIPGRDGFKGEKGECIRESFEESWTNPYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPGANGIPCTPGIPGRDGFKGEKGECIRESFEESWTNPYKQCSWSSLNYGIDL 120

Qy 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180
Db 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180

Qy 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240
Db 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 8
US-10-634-108-4
; Sequence 4, Application US/10634108
; Publication No. US20040063176A1
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard F.
; ATTORNEY: FRISSEL, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Linner et al. (200036..0013)
; CURRENT APPLICATION NUMBER: US/10/644,108
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/10/644,108
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4

Query Match 100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1..6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLQLLQLQDAPSSASEIPKQKAOLQREVVDLYNGMCLQGPA 60
Db 1 MRPOGPAASPORLQLLQLQDAPSSASEIPKQKAOLQREVVDLYNGMCLQGPA 60

Qy 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180
Db 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180

Qy 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240
Db 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240

Qy 241 LPK 243
Db 241 LPK 243

RESULT 9
US-10-188-832-175
; Sequence 175, Application US/10188832
; Publication No. US2004007695A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; ATTORNEY: Aziz, Natasha
; TITLE OF INVENTION: Methods of Bladder Cancer, Compositions
; TITLE OF INVENTION: Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer

Query Match 100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1..6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPOGPAASPORLQLLQLQDAPSSASEIPKQKAOLQREVVDLYNGMCLQGPA 60
Db 1 MRPOGPAASPORLQLLQLQDAPSSASEIPKQKAOLQREVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGSPGANGIPCTPGIPGRDGFKGEKGECIRESFEESWTNPYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPGANGIPCTPGIPGRDGFKGEKGECIRESFEESWTNPYKQCSWSSLNYGIDL 120

Qy 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180
Db 121 GKIACETFTKMRNSALRVLFGSRLKCRNACCRWYFTNGAECSSGPPIEATIYLDQ 180

Qy 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240
Db 181 GSPEMNSTINHRTSSVEGLCEGIGLGLVDAIWTGTCSDYPKGDASTGMNSVRRIEE 240

Qy 241 LPK 243
Db 241 LPK 243

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FILE REFERENCE: 018501-002330US
    CURRENT APPLICATION NUMBER: US10/188, 832
    CURRENT FILING DATE: 2002-11-22
    PRIOR FILING DATE: 2001-07-03
    PRIOR APPLICATION NUMBER: US 60/302, 814
    PRIOR FILING DATE: 2001-08-03
    PRIOR APPLICATION NUMBER: US 60/310, 099
    PRIOR FILING DATE: 2001-11-08
    PRIOR APPLICATION NUMBER: US 60/343, 705
    PRIOR FILING DATE: 2001-11-08
    PRIOR FILING DATE: 2001-11-13
    PRIOR APPLICATION NUMBER: US 60/372, 246
    PRIOR FILING DATE: 2002-04-12
    NUMBER OF SEQ ID NOS: 207
    SOFTWARE: PatentIn Ver. 2.1
    SEQ ID NO: 175
    LENGTH: 243
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-10-188-832-175

Query Match          100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

RESULT 11
US-11-050-926-135
    Sequence 135, Application US/11050926
    Publication No. US20050214831A1
    GENERAL INFORMATION:
        APPLICANT: John MONAHAN
        APPLICANT: Manjula GANNAVARAPU
        APPLICANT: Sebastian HORRSCH
        APPLICANT: Shubhangi KAMATKAR
        APPLICANT: Steve G. KOVATS
        APPLICANT: Rachel E. MEYERS
        APPLICANT: Michael MORRISBY
        APPLICANT: Peter OLANDT
        APPLICANT: Anni SEN
        APPLICANT: Peter VEIBY
        APPLICANT: Gordon B. MILLS
        APPLICANT: Robert C. BAST, Jr.
        APPLICANT: Karen LU
        APPLICANT: Rosemarie SCHMANDT
        APPLICANT: Xumei ZHAO
        APPLICANT: Karen GLATT
    TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
    TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
    FILE REFERENCE: MKI-030
    CURRENT APPLICATION NUMBER: US/11/050, 926
    CURRENT FILING DATE: 2005-02-04
    PRIOR APPLICATION NUMBER: US/10/097, 340
    PRIOR FILING DATE: 2002-03-14
    PRIOR APPLICATION NUMBER: 60/276, 025
    PRIOR FILING DATE: 2001-03-14
    PRIOR APPLICATION NUMBER: 60/325, 149
    PRIOR FILING DATE: 2001-09-26
    PRIOR APPLICATION NUMBER: 60/276, 026
    PRIOR FILING DATE: 2001-03-14
    PRIOR APPLICATION NUMBER: 60/324, 967
    PRIOR FILING DATE: 2001/09/26
    PRIOR APPLICATION NUMBER: 60/311, 732
    PRIOR FILING DATE: 2001-08-10
    PRIOR APPLICATION NUMBER: 60/325, 102
    PRIOR FILING DATE: 2001-09-26
    PRIOR APPLICATION NUMBER: 60/323, 580
    PRIOR FILING DATE: 2001-09-19
    NUMBER OF SEQ ID NOS: 17
    SEQ ID NO: 4
    LENGTH: 243
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-11-050-926-135

Query Match          100.0%; Score 1303; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

RESULT 10
US-10-939-233-4
    Sequence 4, Application US/10939233
    Publication No. US20050147602A1
    GENERAL INFORMATION:
        APPLICANT: LINDNER, Volkhard
        APPLICANT: FRIESER, Robert E.
    TITLE OF INVENTION: METHODS AND KITS RELATING TO CTHRC1, A NOVEL
    TITLE OF INVENTION: MODULATOR OF COLLAGEN MATRIX
    FILE REFERENCE: 033689-5006-03
    CURRENT APPLICATION NUMBER: US/10/939, 233
    CURRENT FILING DATE: 2004-05-10
    PRIOR APPLICATION NUMBER: US 09/692, 081
    PRIOR FILING DATE: 2000-10-19
    PRIOR APPLICATION NUMBER: US 10/045, 992
    PRIOR FILING DATE: 2001-10-19
    NUMBER OF SEQ ID NOS: 17
    SEQ ID NO: 4
    LENGTH: 243
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-10-939-233-4

Query Match          100.0%; Score 1303; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

Query Match          100.0%; Score 1303; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

Query Match          100.0%; Score 1303; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

Query Match          100.0%; Score 1303; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Db          1 MRQQGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          1 MRPOGPAAASPORLGLLILQLQAPSSASEIPKGKOKAOLRQREVDLYNGMCLOGPA 60
Qy          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Db          61 GVPGRDGSPGANGIPGTCGIPGRDGFKCBEKGCLRESPEESWTPNYKOCWSLNYGIDL 120
Qy          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Db          121 GKAECTPKRSNSALVLFSSLRKCRNACQRWYFTENGAECSGPLPIEAYLDQ 180
Qy          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Db          181 GSPEMNSTINHRTSSVFLCEGIGAGLVDAIWVGTCSDYPRGDASTGWNSVRRIEE 240
Qy          241 LPK 243
Db          241 LPK 243

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Best Local Similarity 100.0%; Pred. No. 1.6e-115; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.9e-115; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 MRPQQPAAASPORLRLGLLQLPAPSASBIPKQKAQLRREVVDLYNGMCLQGP 60
Db 1 MRPQQPAAASPORLRLGLLQLPAPSASBIPKQKAQLRREVVDLYNGMCLQGP 60

Qy 61 GVPGRDGS PGANGIPGTPGTPGRDGPKGEKGCLRESFEESWTPNPKQCSWSSLNYGIDL 120
Db 61 GVPGRDGS PGANGIPGTPGTPGRDGPKGEKGCLRESFEESWTPNPKQCSWSSLNYGIDL 120

Qy 121 GKIACETFKRSNSALRVLFSGSLRLKCRNACQWYFTNGAEGSSPPBIAIYLQ 180
Db 121 GKIACETFKRSNSALRVLFSGSLRLKCRNACQWYFTNGAEGSSPPBIAIYLQ 180

Qy 181 GSPEMNSTINHRTSSVEGLECGIGAGLVDVIAIWGTCSDPKGDASTGMNSVRIIEE 240
Db 181 GSPEMNSTINHRTSSVEGLECGIGAGLVDVIAIWGTCSDPKGDASTGMNSVRIIEE 240

Qy 241 LPK 243
Db 241 LPK 243

Qy 241 LPK 243
Db 241 LPK 243

RESULT 13
US-10-177-293-496
Sequence 496, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATIKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, JR.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/275,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 131
LENGTH: 278
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 100.0%; Score 1303; DB 4; Length 278;
US-10-097-340-131

RESULT 13
US-10-177-293-496
Sequence 496, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gamavatpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mervens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoesch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Horobagyi, Gabriel N.
APPLICANT: Pubstai, LaJos
APPLICANT: Meric, Funda
APPLICANT: Sahn, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 496
LENGTH: 278
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 100.0%; Score 1303; DB 4; Length 278;

US-10-177-293-496

Best Local Similarity 100.0%; Pred. No. 1.9e-115; Mismatches 0; Indels 0; Gaps 0;

Matches 243; Conservative 0; Gaps 0;

Qy 1 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 60
Db 36 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 95
Qy 61 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 120
Db 96 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 155
RESULT 15
US-10-296-115-1261
; Sequence 1261, Application US/10296115
; Publication No. US200405324BA1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc.
; TITLE OF INVENTION: NO. US2004005324BA1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784 PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-04-25
; SEQ ID NO: 1261
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1261

Query Match 100.0%; Score 1303; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 60
Db 36 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 95
Qy 61 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 120
Db 96 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 155
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TREATMENT OF COLON CANCER
; FILE REFERENCE: MPN01-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 77
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-301-822-77

Query Match 100.0%; Score 1303; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 60
Db 36 MRPGDGPSPQRGLLQLQLPAPSASETPKGOKAQLREVDLNLNGMCLQGP 95
Qy 61 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 120
Db 96 GVPGRDGSPGANGIPGTGIPGRDGFKBKGCLRESFEESPTNYKQCSWSSLNLYGIDL 155
Qy 121 GKIAECKPTKRSNSALRVLFGSSLRKCRNAACQRYFTENGACSGPLPEAIIYLDQ 180
Db 156 GKIAECKPTKRSNSALRVLFGSSLRKCRNAACQRYFTENGACSGPLPEAIIYLDQ 215
; Search completed: April 20, 2006, 09:56:57
; Job time : 94.1176 secs

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